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(54) Title: EXPRESSION TECHNOLOGY FOR PROTEINS CONTAINING A HYBRID ISOTYPE ANTIBODY MOIETY

(57) Abstract: Disclosed are methods and compositions for efficiently expressing antibody fusion proteins. Antibody fusion pro-
teins of the invention include a hybrid antibody moiety containing sequences from more than one type of antibody and/or mutant
antibody sequences. Hybrid antibody fusion proteins of the invention may be produced at high levels and may combine functional
properties characteristic of different antibody types in addition to functional properties of a non-antibody moiety.

EXPRESSION TECHNOLOGY FOR PROTEINS CONTAINING A HYBRID ISOTYPE ANTIBODY MOIETY

Related Applications

[0001]   This application claims priority to, and the benefit of U.S.S.N. 60/274,096
5   filed March 7, 2001, the disclosure of which is incorporated by reference herein in its
entirety.

Field of the Invention

[0002]   The present invention relates generally to methods and compositions for
antibodies with moieties deriving from two or more isotypes, and fusion proteins
10   derived therefrom, including proteins containing an antibody moiety with altered
effector functions, increased protein expression and/or decreased oligomerization.
The invention particularly relates to antibodies and fusion proteins in which a hinge
region derives from one isotype and the CH2 domain derives from a different isotype.

Background of the Invention

15   [0003]   The efficiency of protein expression from genetically engineered cells is
an important commercial concern. Some commercially important proteins are best
made from eukaryotic cells, such as mammalian cells, plant cells, or yeast cells, in
order to ensure correct folding and glycosylation. However, the cost of maintaining
large cultures of eukaryotic cells means that proteins produced in this way are
20   expensive to make. Therefore, there is a need in the art to maximize the expression
levels of proteins from eukaryotic cells.

[0004]   A related issue is that therapeutic proteins produced from eukaryotic cells
must be expressed in the correct conformational state. Normally, mechanisms of
transcription and translation ensure that a genetically engineered cell will produce a
25   protein whose sequence is determined by the nucleic acid encoding the protein.
However, after transcription and translation, the protein may fail to fold properly and
may be degraded. Alternatively, a protein may be produced in an aggregated state,
such that activity is reduced. Even if an aggregated protein is active, it may be
pharmacologically unacceptable due to increased immunogenicity compared to a non-
30   aggregated protein. Thus, a pharmacologically acceptable protein preparation should
generally be substantially free of aggregated proteins.

[0005]   The amount of a protein that is expressed from a genetically engineered eukaryotic cell is a function of the rate of transcription of the encoding gene, the efficiency of mRNA splicing and of export from the nucleus, and the efficiency of translation. The role that these events play in protein expression is sufficiently well

5   understood that one skilled in the art of genetic engineering and protein expression can generally incorporate appropriate nucleic acid sequences into the design of an expression construct with efficient transcription, splicing, mRNA export, and translation.

[0006]   However, the amount of a correctly folded, non-aggregated protein that is

10   produced from a eukaryotic cell is also a function of the amino acid sequence of the protein, as well as the nucleic acid sequences that determine transcription, splicing, mRNA export, translation, and post-translational modification. For example, it is thought that a significant fraction of proteins synthesized in a cell is degraded. The features in a protein that determine whether or not it should be degraded are currently

15   subject to intensive study, but presently it is not possible to predict the efficiency of protein folding, degradation, or aggregation by simply examining the sequence of a protein. Some naturally occurring proteins fold efficiently, are resistant to proteolysis, and do not aggregate. In contrast, other proteins fold inefficiently, are rapidly degraded, and aggregate.

20   [0007]   Antibodies and artificial proteins containing a portion of an antibody, termed antibody fusion proteins or Ig fusion proteins herein, are useful for a variety of purposes relating to the targeting capability of antibody variable domains as well as the ability of the constant regions to bind to various other proteins. Antibody and antibody fusion protein preparations are particularly useful when they are correctly

25   folded and non-aggregated. Therefore there is a need in the art for methods and compositions for the production of antibody and antibody fusion protein preparations with reduced aggregation.

[0008]   Additionally, antibodies and antibody fusion proteins are useful since their ability to bind to various other proteins enables them, for example, to elicit specific

30   effector functions. In some instances specific effector functions are desirable but often the loss of effector functions is preferable. The antibody component of a fusion protein may be altered to reduce or eliminate effector functions by utilizing a modified antibody. Antibody and antibody fusion protein preparations are also useful

when they are modified to alter functionality. Therefore there is a need in the art for methods and compositions for the production of modified antibodies and antibody fusion proteins with altered effector functions.

[0009]   Protein drugs can be degraded by proteases, such that their delivery and pharmacokinetic properties are suboptimal. There is a need in the art for improvement of protein drugs that have the useful properties of certain proteins, but that have greater protease resistance.

Summary of the Invention

[0010]   The present invention features methods and compositions useful for producing intact antibodies, immunocytokines, immunofusins, immunoligands, and other antibody and Fc fusion proteins that enhance the expression, proper oligomerization, purification, and protease resistance of a desired fusion protein optionally with modified, combined, or decreased Fc effector functions. Specifically, the invention provides antibody moieties with hybrid isotypes, optionally using mutant Ig components for use in intact antibodies and in fusion proteins containing an antibody moiety.

IgG/IgG hybrid isotypes

[0011]   In one set of preferred embodiments, the invention provides fusion proteins with decreased effector functions and improved assembly. Such fusion proteins are particularly useful when the Ig moiety serves to enhance expression and improve serum half-life, but when the immunological functions of the Ig moiety are not needed.

[0012]   In these embodiments, the fusion protein preferably comprises CH1, CH2, and/or CH3 domains of an IgG2 or IgG4, combined with a hinge region from IgG1 or a hinge region from IgG4, the latter hinge region preferentially comprising a mutation that enhances correct formation of disulfide bonds between heavy chain-derived moieties (Angal S, et al. Mol Immunol 1993 Jan;30(1):105-8). Fusion proteins of this embodiment facilitate high-level expression and improve the correct assembly of intact antibodies and Ig fusion proteins containing Fc regions.

[0013]   In a more preferred embodiment, the fusion proteins also contain one or more mutations in the Ig moiety. For example, the Ig moiety is mutated to further

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reduce any remaining effector function that is not desired. For example, the C1q binding site in the CH2 domain of IgG2 is mutant. For example, normal IgG4 does not bind complement because it contains a serine instead of a corresponding proline at position 331 in IgG1 (Eu nomenclature)(Tao, MA et al (1993) J. Exp. Med. 178:661-

5   667; Brekke, OH et al (1994) Eur. J. Immunol. 24:2542-2547); a similar mutation in IgG2 reduces C1q binding. Other residues known to be involved in C1q binding could be modified such as residues at positions 318, 320, 322 and 297 (Duncan AR (1988) Nature: 332:738-740), resulting in a decrease in C1q binding.

[0014]   In another set of preferred embodiments, a mutation in the hinge region is

10   also present. For example, in cases where an antibody light chain is also present, a form of an IgG1 hinge region with the cysteine residues in the normal number at their normal positions is preferred. However, in cases where an antibody light chain is not present as a distinct polypeptide chain, an IgG1 hinge in which the first cysteine is mutated to another residue is preferred. For example, it is useful to employ such a

15   mutated hinge region in Fc-X proteins, X-Fc proteins, and in single-chain antibodies in which the light chain variable region is attached to the heavy chain by means of a polypeptide linker. The first cysteine in the IgG1 hinge is preferably mutated to a serine in this context.

[0015]   In a second class of embodiments involving a mutant hinge region, a

20   mutant form of the IgG4 hinge that allows efficient disulfide bonding between the two heavy chains is used.

[0016]   In a third class of embodiments involving a mutant hinge region, a mutant form of the IgG2 hinge, in which the first two cysteines are each mutated to another amino acid, is used in a hybrid isotype antibody or Ig fusion protein. It is also

25   convenient to use such a mutant hinge in an antibody or Ig fusion protein that is entirely derived from IgG2. For example, a modified IgG2 hinge with the sequence ERKSSVECPPCP (SEQ ID NO: 1) is used in the context of an antibody or Ig fusion protein. Another useful type of hinge is a hybrid between the IgG2 hinge and the IgG4 hinge, such as the sequence ESKYG-VECPPCP (SEQ ID NO: 2), in which the 5

30   amino acids before the dash are derived from IgG4 and the remaining amino acids are from IgG2. These embodiments are particularly useful in the context of antibodies and Ig fusion proteins expressed and secreted from eukaryotic cells, because these hinge embodiments promote correct assembly of the proteins. These embodiments

may be used as an alternative to the IgG1 hinge. A key feature of these embodiments of an antibody hinge is that they only have two cysteine residues.

[0017]   Yet another class of embodiments involve mutations in the Ig moiety of hybrid isotype Ig fusion proteins at the junction between the Ig and non-Ig moieties. In one embodiment, the alterations in the amino acid sequence of the fusion protein are preferentially at the junction of the Ig moiety and the non-Ig moiety and preferably lie within 10 amino acids of the junction point. More preferably, the amino acid changes involve changing the C-terminal lysine of the antibody moiety to a hydrophobic amino acid such as alanine or leucine.

[0018]   An alternative embodiment is useful in circumstances where it is desirable to shorten the half-life of a fusion protein. IgG3 has a short half-life relative to other IgG isotypes due to a modification in the FcRn/FcRp binding site located in the CH3 domain (H435 to R)(see Ward, ES. and Gheti, V [1995] Therapeutic Immunology 2:77-94). A fusion protein with IgG3 CH2 and CH3 domains may be used when short term exposure is desirable. According to this embodiment, it is useful to use an IgG3 CH3 domain in combination with an IgG1 hinge; such an IgG1(hinge)-IgG3(CH3) fusion protein has superior expression and assembly properties compared to an Ig fusion protein containing an IgG3 hinge and an IgG3 CH3 domain.

[0019]   In a more preferred embodiment of an Ig fusion protein designed to have a short serum half-life, reduced effector functions, and efficient assembly, a hybrid Ig region is used in which the hinge region derives from IgG1, the CH2 domain derives from IgG2, and the CH3 domain derives from IgG3.

IgG/IgA hybrid isotypes

[0020]   A distinct embodiment of the invention provides hybrid isotype Ig fusion proteins with enhanced protease resistance and enhanced serum half-life. This embodiment is particularly useful in situations in which an Ig fusion protein is exposed to an environment rich in proteases, such as the gut or another mucosal tissue, for example during oral delivery of a Ig fusion protein drug. According to this embodiment, an Ig fusion protein containing elements of the IgG and IgA constant regions is provided. In a preferred embodiment, the hinge of IgA1 and the CH2 and CH3 domains of an IgG are used. In a distinct preferred embodiment, the segments of

amino acids encoding the O-linked glycosylation sites in the Fc region of IgA are grafted into the Fc region of an IgG.

IgG/IgM hybrid isotypes

5   [0021]   Yet another embodiment of the invention provides hybrid isotype antibodies and Ig fusion proteins with oligomerization features of IgA or IgM but with effector functions characteristic of IgG. For example, a protein comprising the hinge region and CH2 domain of IgG1 or IgG3 fused to the CH3 and CH4 domain of IgM is provided. In a more preferred embodiment, an antibody comprising heavy and

10   light chain variable regions and also comprising an IgG hinge and CH2 region fused to the CH3 and CH4 domain of IgM is provided. In an alternative more preferred embodiment, an Ig fusion protein of the form X-Fc is provided, in which X is preferably a ligand for a cell-surface receptor, and the Fc moiety comprises the CH3 and CH4 domain of IgM. Such a molecule combines the ADCC effector function of

15   an IgG with the high valency of IgM.

[0022]   In a preferred embodiment of a hybrid isotypes using the CH4 domain of IgM or IgA, the C-terminal cysteine in the CH4 domain is mutated to block disulfide bonding to the J chain. This reduces secretion of the Ig fusion protein into the gut.

20   *Preferred non-Ig moieties*

[0023]   The preferred type of non-Ig moiety in the fusion proteins of the invention is a protein or moiety that is normally extracellular when not part of an Ig fusion protein. For example, a hormone, cytokine, chemokine, secreted enzyme, or extracellular portion of a trans-membrane receptor.

25   [0024]   In a preferred embodiment, the non-immunoglobulin component is a protein such as an anti-obesity protein. For example, the non-immunoglobulin component is leptin, CNTF, CLC/CLF-1 or a portion of Acrp30.

[0025]   In yet another preferred embodiment, the non-immunoglobulin component is a protein such as erythropoeitin or EPO.

30   [0026]   In an alternative embodiment, the non-immunoglobulin component of the fusion protein is a hormone. For example, the non-immunoglobulin component may be insulin, growth hormone, or glucagon-like peptide 1(GLP-1).

[0027]   In another embodiment, the non-immunoglobulin component of the fusion protein is a cytokine. The term "cytokine" is used herein to describe naturally occurring or recombinant proteins, analogs thereof, and fragments thereof that elicit a specific response in a cell which has a receptor for that cytokine. Preferably cytokines are proteins that may be produced and secreted by a cell. Preferably, cytokines include interleukins such as interleukin-2 (IL-2), IL-4, IL-5, IL-6, IL-7, IL-10, IL-12, IL-13, IL-14, IL-15, IL-16 and IL-18, hematopoietic factors such as granulocyte-macrophage colony stimulating factor (GM-CSF), G-CSF and erythropoietin, tumor necrosis factors (TNF) such as TNFα, lymphokines such as lymphotoxin, regulators of metabolic processes such as leptin, interferons such as interferon α, interferon β, and interferon γ, and chemokines. Preferably, the Ig-cytokine fusion protein of the present invention displays cytokine biological activity.

[0028]   In an alternative preferred embodiment, the non-immunoglobulin component of the fusion protein is a ligand-binding protein with biological activity. Such ligand-binding proteins may, for example, (1) block receptor-ligand interactions at the cell surface; or (2) neutralize the biological activity of a molecule (e.g., a cytokine) in the fluid phase of the blood, thereby preventing it from reaching its cellular target. Preferred ligand-binding proteins include CD4, CTLA-4, TNF receptors, or interleukin receptors such as the IL-1 and IL-4 receptors. Preferably, the antibody-receptor fusion protein of the present invention displays the biological activity of the ligand-binding protein. One highly preferred embodiment comprises the extracellular TNF-receptor domain fragment used in the protein drug Enbrel, in the format TNFR-hinge-CH2-CH3 or hinge-CH2-CH3-TNFR, in which the CH2 and CH3 domains are derived from IgG2 or IgG4 and each of the two hinge regions in the dimeric Fc has three or fewer cysteines, and even more preferably, two or fewer cysteines.

[0029]   Another type of preferred ligand-binding protein has the capacity to bind to small molecules rather than proteins. For example, it is convenient to fuse avidin to a hybrid isotype Ig moiety, such as an antibody. The hybrid isotype antibody-avidin fusion is then administered to a mammal such as a mouse or human and becomes concentrated in a target tissue of the body, as determined by the specificity of a V region of the antibody. After the antibody-avidin fusion protein has sufficiently cleared from the body, a conjugate of biotin and a therapeutic molecule is

administered. The biotin conjugate becomes concentrated in the target tissue by
virtue of binding to avidin, which results in a lessening of side effects that could arise
from a concentration of the therapeutic molecule in non-target tissues. This strategy
can be used with other ligand/ligand-binding protein pairs.

5   [0030]   Another type of preferred non-immunoglobulin moiety is an enzyme. For
example, an enzyme with a distinctive specificity may be fused to a hybrid isotype Ig
moiety, such as an antibody. The hybrid isotype antibody-enzyme fusion is then
administered to a mammal such as a mouse or human and becomes concentrated in a
target tissue of the body, as determined by the specificity of a V region of the

10   antibody. In one preferred treatment method of the invention, after the antibody-
enzyme fusion protein has sufficiently cleared from the body, a prodrug that can be
cleaved into an active form by the enzyme is administered. The activated drug
becomes concentrated in the target tissue, which results in a lessening of side effects
that could arise from a concentration of the activated drug molecule in non-target .

15   tissues. In a highly preferred form of this embodiment, the activated drug is an
anticancer drug, such as a cytotoxic agent. In an alternative highly preferred
embodiment, the enzyme itself has a therapeutic activity. For example, an RNAse
such as Onconase is coupled to a hybrid isotype antibody fusion protein and targeted
to a tumor via an antibody V region.

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Nucleic acids

[0031]   This invention also provides novel nucleic acid sequences that facilitate
the expression and secretion of Ig fusion proteins and intact antibodies with hybrid
isotypes, as well as methods for the construction of such nucleic acids.

25   [0032]   A particularly useful feature of genomic sequences encoding antibody
proteins is that the variable region, CH1, hinge, CH2, CH3, and CH4 regions are
encoded by separate exons. This feature facilitates the engineering of hybrid isotype
Ig fusion proteins by 'exon shuffling' (Zuckier et al., Cancer Research [1998]
58:3905-8; Poon et al., J. Biol. Chem. [1995] 270:8571-7; Jefferis R, et al., Mol

30   Immunol.[1990] 27:1237-40; Chappel MS, Proc Natl Acad Sci U S A. [1991]
88:9036-40; Senior BW, et al., Infect Immun. [2000] 68:463-9.).

[0033] For Fc fusion proteins, nucleic acid molecules can encode the protein in various configurations. In a preferred set of embodiments, a nucleic acid molecule encodes, serially in a 5' to 3' direction, (i) a signal sequence, an immunoglobulin Fc region and a target protein sequence or (ii) a signal sequence, a target protein, and an immunoglobulin Fc region, or (iii) a signal sequence, a first target protein, an immunoglobulin Fc region, and a second target protein. The resulting nucleic acid molecule thereby encodes an Fc-X, X-Fc, or X-Fc-Y structure where X and Y are a target protein or proteins. For example, X and Y may themselves be fusion proteins. Linkers are optionally encoded between these moieties.

[0034] Similarly, according to the invention, nucleic acids encoding whole antibody Ig fusion proteins are designed to encode a signal sequence at the N-terminus of each heavy chain moiety and each light chain moiety.

[0035] A nucleic acid of the invention can be incorporated in functional association into a replicable expression vector which can then be introduced into a eukaryotic host cell competent to produce a fusion protein. The resultant Ig fusion proteins are produced efficiently and secreted from the eukaryotic host cells. Secreted Ig fusion proteins may be collected from the culture media without lysing the eukaryotic host cell. The protein product can be assayed for activity and/or purified using common reagents as desired, and/or cleaved from the fusion partner, all using conventional techniques. Alternatively, a nucleic acid of the invention may be introduced into a bacterial cell, and the resulting Ig fusion protein purified according to standard techniques.

[0036] The invention also provides methods of enhancing the levels of antibodies and Ig fusion proteins produced in cells. The method is preferably applied to production in eukaryotic cells, preferably mammalian cells. For example, according to the method, the production of a starting antibody or Ig fusion protein is improved by exchanging nucleic acid sequences encoding domains of the Ig moiety with corresponding sequences encoding domains from other antibody isotypes, or with mutant sequences, comparing expression levels by assaying the production of the altered protein as described herein, and choosing particular expression constructs that give the highest levels. This process may be used iteratively. It is particularly useful to interchange hinge regions.

Treatment

[0037]   The invention also provides methods of treatment using the modified antibodies and Ig fusion proteins. Accordingly, the invention provides processes that are both efficient and inexpensive as well as proteins that are less immunogenic.

5   [0038]   The foregoing and other objects, features and advantages of the present invention will be made more apparent from the detailed description, drawings, and claims that follow.

Brief Description of the Drawings

10   [0039]   Figures 1A-D are schematic illustrations of IgG hybrid isotypes used to prepare fusion proteins in accordance with certain aspects of the invention; the thick lines represent disulfide bonds connecting cysteine residues; antibody domains are indicated in Figure A; IgG1 domains are shown in black, IgG2 domains are shown in white, and variable and light chain domains are shown striped.

15   [0040]   Figure 1A shows an IgG1 isotype.

[0041]   Figure 1B shows an IgG2 isotype.

[0042]   Figure 1C shows an isotype hybrid with an IgG2 and an IgG1 hinge having a mutation of the first cysteine.

[0043]   Figure 1D shows an IgG hybrid $\gamma1(CH1-H)$ $\gamma2(CH2-CH3)$.

20   [0044]   Figures 2A-C are schematic illustrations of Ig fusion proteins comprising Fc regions that contain hybrid isotypes; "X" and "Y" may be any non-Ig moiety.

[0045]   Figure 2A shows an Ig fusion protein in the Fc-X configuration comprising a hinge from one antibody isotype and an Fc moiety consisting of a CH2 and CH3 domain from a second isotype; at the C-terminus of the Fc moiety is a

25   protein moiety "X".

[0046]   Figure 2B shows an Ig fusion protein in the X-Fc configuration comprising a hinge from one antibody isotype and an Fc moiety consisting of a CH2 and CH3 domain from a second isotype; at the N-terminus of the Fc moiety is a protein moiety "X".

30   [0047]   Figure 2C shows an Ig fusion protein in the X-Fc-Y configuration comprising a hinge from one antibody isotype and an Fc moiety consisting of a CH2

and CH3 domain from a second isotype; at the N-terminus of the Fc moiety is "X", which can be any protein, and at the C-terminus of the Fc moiety is a protein moiety "Y".

[0048]   Figures 3A-D are schematic illustrations of Ig fusion proteins that comprise variable regions and that contain hybrid isotypes; "X" and "Y" may be any non-Ig moiety.

[0049]   Figure 3A shows an Ig fusion protein comprising a hinge from one antibody isotype (black) and CH1, CH2, and CH3 regions from a different isotype; a non-Ig protein "X" is fused at the C-terminus of the heavy chain.

[0050]   Figure 3B shows an Ig fusion protein comprising a hinge from one antibody isotype (black) and CH1, CH2, and CH3 regions from a different isotype; a non-Ig protein "X" is fused at the C-terminus of the heavy chain; arrows indicate a subset of possible sites of mutation in the antibody moiety, as described herein.

[0051]   Figure 3C shows an Ig fusion protein comprising a hinge and a CH1 region from one antibody isotype (black) and CH2, and CH3 regions from a different isotype; a non-Ig protein "X" is fused at the C-terminus of the heavy chain; the branched structure emanating from the hinge represents a glycosylation moiety.

[0052]   Figure 3D shows an Ig fusion protein comprising a hinge from one antibody isotype (black) and CH1, CH2, and CH3 regions from a different isotype; a non-Ig protein "X" is fused at the C-terminus of the heavy chain; a second non-Ig protein "Y" is fused at the N-terminus of the light chain.

[0053]   Figure 3E shows an Ig fusion protein comprising a hinge from one antibody isotype (black) and CH1, CH2, and CH3 regions from a different isotype; a non-Ig protein "X" is fused at the C-terminus of the heavy chain; a second non-Ig protein "Y" is fused at the N-terminus of the heavy chain.

[0054]   Figure 4 is a schematic illustration of an Ig fusion protein that comprises variable regions, comprising multiple isotypes, and that have increased valency compared to IgG; black ovals represent the CH3 and CH4 domains from IgM; white ovals represent the CH1, hinge, and CH2 domains from an IgG; striped ovals represent variable domains and the light chain constant domain; thick lines represent disulfide bonds normally found in IgG1; thin lines labeled with an 's' represent disulfide bonds normally found in IgM.

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Definitions

[0055]   According to the invention, by isotype is meant the class of heavy chain constant (C) region of an immunoglobulin which determines the functional activity of an antibody. There are five major classes including IgA, IgG, IgM, IgD, and IgE.

5   By IgA is meant the class of immunoglobulin characterized by α heavy chains.

By IgD is meant the class of immunoglobulin characterized by δ heavy chains.

By IgE is meant the class of immunoglobulin characterized by ϵ heavy chains.

By IgM is meant the class of immunoglobulin characterized by μ heavy chains.

By IgG is meant the class of immunoglobulin characterized by γ heavy chains.

10   "Gamma1" or "γ1" refers to a heavy chain or portion thereof derived from an IgG1. Similarly, "gamma2" or "γ2" derives from IgG2, and so on.

[0056]   According to the invention, by allotype is meant allelic polymorphisms of the same heavy chain C gene of an immunoglobulin. These determinants are found in some, but not all, members of a species.

15   [0057]   According to the invention, by idiotype is meant antigenic determinants found on the variable (V) regions of antibodies and are due to particular rearranged V_H and V_L genes.

[0058]   According to the invention, by FcRn, also know as FcRp, is meant the beta-2 microglobulin-containing neonatal intestinal transport receptor which regulates
20   the clearance of IgG and is important for the *in vivo* circulating half-life of antibodies.

[0059]   According to the invention, by FcγR is meant cell surface receptors, including FcγRI, RII, and RIII, that bind the Fc portion of IgG molecules and elicit effector cell functions. FcγR are expressed on phagocytes, B lymphocytes, NK cells and dendritic cells.

25   [0060]   According to the invention, by "an IgG1," or "IgG2," or other Ig molecule is meant a whole antibody including a heavy and light chain, or a portion thereof.

[0061]   According to the invention, by "a bivalent monomer" is meant an antibody, Fc fusion, or antibody fusion that is normally dime: :zed by the formation of disulfide bonds that form in a normal antibody. The formation of such disulfide
30   bonds is generally inferred by the ability of an Fc-containing protein to migrate on a denaturing, non-reducing SDS gel as a single band with an apparent molecular weight

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about twice that of the apparent molecular weight seen with reducing conditions. The presence of a bivalent monomer is also inferred by the presence of a peak in a size exclusion chromatograph that corresponds to the correct molecular weight. Other protein sizing methods may also be used to identify the presence of bivalent

5   monomers.

[0062]   According to the invention, by "an Ig fusion protein" is meant a fusion protein that contains part or all of an antibody linked to a second moiety which is preferably part or all of a non-antibody or non-immunoglobulin (non-Ig) protein. Immunocytokines, Fc-X proteins, X-Fc proteins, and X-Fc-Y proteins are all

10   examples of Ig fusion proteins. Similarly, fusion proteins in which a non-Ig moiety is placed between two Ig moieties or domains constitute a type of Ig fusion protein.

[0063]   According to the invention, by "assembly" of a protein is meant the proper folding of a protein and oligomerization into a correct multimeric state. Assembly can be monitored in many ways that are established in the art. In practice, correct

15   assembly of a protein, with respect to disulfide bonds, can be conveniently monitored by comparing migration on a non-reducing and reducing SDS gel: if a given protein species forms multiple bands on a non-reducing gel, but forms a single band on a reducing SDS gel, it can be inferred that at most only one of the bands on the non-reducing SDS gel is the correctly assembled species. Alternatively, size exclusion

20   chromatography can be used to distinguish unit proteins from higher-order oligomers and aggregates that may form from incorrect disulfide bonding or non-covalent interactions.

[0064]   According to the invention, by "domain" of an antibody moiety is meant a structural domain that corresponds to the amino acid segments encoded by individual

25   exons in antibody genes in humans. For example, the constant domains of an IgG are the CH1, hinge, CH2, and CH3 domains. In some cases, the hinge and CH2 domains are encoded by the same exon. In such cases, a junction between the hinge and CH2 domain is defined by alignment with other hinge/CH2 junctions (see Paul , op cit., p. 46-49).

30   [0065]   According to the invention, by domain, protein, region, or molecule is meant an entire domain, protein, region, or molecule, or a portion, mutant or engineered form thereof, or a form principally derived therefrom. The portion,

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mutant, or engineered form preferably has functional properties characteristic of the entire domain, protein, region, or molecule. According to the invention, by "principally deriving" is meant having at least 95% of its amino acids deriving from a particular sequence of a naturally occurring protein or domain. For example, a sequence that principally derives from the human IgG2 CH2 domain is at least 95% identical to human IgG2 CH2 domain in an amino acid alignment.

[0066]   According to the invention, by "modified IgG1 hinge" is meant a hinge region from IgG1 in which a cysteine, preferably the first cysteine is mutated to another amino acid. This cysteine normally forms a disulfide bond to the antibody light chain. The modified IgG1 hinge is particularly useful in proteins that either lack the light chain or that have another cysteine that can bond to the light chain.

[0067]   According to the invention, by "an erythropoietin molecule" is meant a molecule that has generally the same structure and similar amino acid sequence to a vertebrate erythropoietin, optionally including mutations. For example, Example 18 describes the use of human erythropoietin without mutations and of a version of human erythropoietin with four mutations.

Detailed Description of the Invention

[0068]   The present invention provides methods and compositions for improving the *in vivo* and *in vitro* production of immunoglobulin fusion proteins. In particular, the invention provides useful methods for improving the expression, aggregation, and/or folding properties of immunoglobulin fusion proteins. The invention is based in part on the surprising observation that an immunoglobulin fusion protein is expressed at a higher level, with fewer aggregation and/or folding problems, when a hybrid immunoglobulin is used as the fusion partner instead of a wild-type immunoglobulin. The improved fusion protein production properties associated with hybrid immunoglobulins are unexpected since wild-type immunoglobulins such as IgG1 and IgG2 are thought to be well folded proteins that are expressed efficiently both *in vivo* and *in vitro*.

[0069]   Accordingly, one aspect of the invention includes methods and compositions useful for expressing immunoglobulin fusion proteins that include a hybrid immunoglobulin (or hybrid Ig) moiety. Preferred hybrid immunoglobulins

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include an IgG1 hinge and an IgG2 CH2 and CH3 domains. Other preferred hybrids include IgG1 and IgG4 domains.

Antibody structure

5   [0070]   Antibodies are Y shaped molecules and are composed of two heavy (H) and two light (L) chains. Each heavy chain is linked to a light chain by a disulfide bond and relies on covalent and noncovalent interactions to properly orient the two chains relative to each other. The variable domains at the amino termini of these two chains contain the antigen-binding site and, with the CH1 domains, define the Fab end

10   of the molecule.

[0071]   The four chains use hydrophobic bonding between the heavy chains and one or more interchain disulfide bonds to stabilize the complex. Thus the complete immunoglobulin is bivalent with two identical antigen-binding sites. Certain immunoglobulins normally undergo additional multimerization, such as IgM and IgA.

15   [0072]   Each polypeptide chain has two to five domains; the light chains contain two domains while the heavy chains contain four or five. The single amino terminal domain of each chain is termed variable due to extensive sequence variation, while the several carboxy-terminal domains are referred to as the constant regions. Heavy chain regions are numbered CH1, hinge, CH2, CH3, CH4 and are responsible for

20   many important antibody functions including Fc receptor (FcR) binding and complement fixation.

[0073]   There are five major isotype classes of heavy chain C regions, classified as IgA, IgG, IgD, IgE, IgM, each with characteristic effector functions (IgG is separated into four γ isotype subclasses: γ1, γ2, γ3, γ4). The constant regions of the light chain

25   possess only one C domain and can be one of the two classes, Ck and Cλ, which have no known distinct functional attributes (see, W. E. Paul, ed., 1993, Fundamental Immunology, Raven Press, New York, N.Y).

[0074]   All immunoglobulins have a hinge region located C terminal to the CH1 domain of their heavy chains separating the Fab and Fc regions of the molecule. In

30   most cases, the hinge regions permit a large degree of flexibility between the antigen binding (Fab end) and effector-interaction (Fc) components of the molecule, thereby linking the two key functional elements of the antibody. In the IgG isotypes,

interchain disulfide bonds typically form within this hinge region, generating the final
tetrameric molecule.

[0075]   Except for IgM, the hinge region is dominated by prolines, serines and
threonines, amino acids that tend to prevent formation of secondary structures and
that are thought to give hinges flexibility. The IgG1 isotype, often used for fusion
proteins, has two disulfide bonds in the hinge region that link the heavy chains to one
another. In contrast, the IgG2 isotype has four disulfide bonds (Figure 1). According
to the invention, these disulfide bonds tend to promote incorrect assembly of
antibodies and Ig fusion proteins, as shown in the unexpected findings in the
Examples.

Useful configurations of Ig fusion proteins

[0076]   Immunocytokines are only one example of a tumor-targeted fusion protein
therapy for which methods and compositions of the invention are useful. Other
tumor-toxic molecules may also be targeted to tumors by fusion to tumor-specific
antibodies according to the invention. In addition, other types of diseased cells, such
as virus-infected cells, may be attacked by antibody fusion proteins according to the
invention.

[0077]   Methods and compositions of the invention are also useful in combination
with the use of Fc-X and X-Fc technology. According to the invention, the use of
hybrid antibody isotypes in a fusion protein further improves the production and
collection of a target protein or polypeptide of interest that is linked to the Fc portion
of an immunoglobulin. For Fc-X fusion proteins, a signal peptide, followed by the Fc
fragment of an immunoglobulin gene is the N-terminal fusion partner to the target
protein. The fusion protein is then expressed in a host cell, for example a mammalian
cell such as a cell that naturally expresses the immunoglobulin. The signal peptide-Fc
fragment in the a N-terminal fusion partner directs the target protein through the
secretory pathway such that the fusion protein is readily secreted. Additionally, use
of the Fc fragment, which is normally glycosylated and highly charged at neutral pH,
facilitates solubilization of more hydrophobic proteins. The targeting of Fc-X fusion
proteins through the secretory pathway also alleviates problems associated with
protein toxicity inside the cell and facilitates the isolation of stable cell lines. The
fusion protein product is easily assayed and purified as it is readily collected from the

culture media in its native conformation with retention of both biological and enzymatic activities. The efficacy of this technology has been demonstrated with Fc-leptin and Fc-erythropoietin. Some of these advantages are also inherent in X-Fc proteins.

5   [0078]   According to the invention, examples of useful fusions of antibody moieties include Fc-X, X-Fc, and X-Fc-Y proteins. Such proteins contain an Fc region with a non-antibody protein or protein fragment fused at the N-terminus, the C-terminus, or both the N-terminus and C-terminus. One advantageous effect of fusion to the Fc region is that the serum half-life of the fusion partner can be significantly

10   extended. A second advantageous effect is that an 'X' can be effectively dimerized by attachment to the Fc. For example, Enbrel is a fusion protein consisting of a portion of a TNF receptor and a human IgG1 Fc region.

[0079]   In some embodiments of the invention, it is specifically advantageous to engineer a fusion protein with hybrid isotypes in the X-Fc orientation. With these

15   constructs the target protein is the N-terminal fusion protein and the Fc fragment follows. For some proteins this approach may be useful, for example with lymphocyte cell surface glycoprotein (LHR) (see US patent 5,428,130).

[0080]   According to the invention, the utility of recombinant antibody-based fusion proteins, albeit better than protein or cytokine treatments alone, may be limited

20   by their rapid *in vivo* clearance from the circulation since antibody fusion proteins have a significantly lower *in vivo* circulating half-life than the free antibody. The decreased circulating half-life is likely a result of increased clearance via the Fc receptor (FcR). Switching of isotype has proven to be one mechanism by which features such as half-life can be altered. Improvements in the half-lives of two

25   immunocytokines have been demonstrated (Cancer Research 59(9):2159-66, 1999) by changing the isotype of the human heavy chain C region from IgGγ1 or IgG γ3 to IgG γ4, an isotype with reduced FcR binding. The IgG4-based immunocytokines and fusion proteins have 10-fold reduced FcR binding and reduced Fc receptor effector functions such as ADCC, but still show similar or better efficacy in mouse tumor

30   models than that of the original IgGγ1 based fusion proteins. However, the invention provides fusion proteins based on hybrid antibodies that combine functional and structured properties of different antibody types in a single molecule.

[0081]   Accordingly, for certain applications, the IgG2 isotype confers superior qualities to the antibody fusion protein since the IgG2 isotype has greatly reduced Fc receptor binding (Hulett et al. [1994] Adv. Immunol.57:1127). As with whole antibody fusion proteins, it is sometimes advantageous to use a γ2 isotype in fusion

5   proteins containing only an Fc region. The rationale is the same as for whole antibodies: it is often desirable to avoid the binding to Fc receptors that is mediated by Fc regions derived from other isotypes.

[0082]   However, the use of the IgG2 isotype in a fusion protein generally causes some level of inappropriate assembly, as described herein. Methods and

10   compositions of the invention provide antibody fusion proteins that have the minimized effector functions of the IgG2 isotype, but which do not have the aggregation properties of this isotype.

[0083]   According to the invention, novel hybrid isotype antibodies and fusion proteins show enhanced expression and improved assembly over that of IgG2-based

15   fusion proteins. Additionally, hybrid isotype antibodies and fusion proteins may have increased efficacy in therapeutics where Fc receptor effector functions are not desired.

Types of Hinges

[0084]   Hybrid isotype antibodies of the invention also include antibodies wherein

20   the hinge region is a mutant hinge region, preferably a hinge region with a reduced number of cysteine residues, for example, a modified IgG1 hinge region in which the first cysteine is mutated to serine. The first cysteine of the IgG1 hinge region normally bonds to the light chain. In an Fc-X protein or an X-Fc protein or any other antibody fusion protein lacking a light chain, this cysteine does not serve its natural

25   function and therefore can be mutated. However, according to the invention, a hybrid isotype antibody with an IgG1 hinge missing the first cysteine and an IgG2 CH1 domain can associate with a light chain, because the light chain normally forms a disulfide bond with a cysteine within the IgG2 CH1 domain. The four cysteines within the IgG2 hinge are thought to form disulfide bonds with each other.

30   [0085]   According to the invention, the cysteines in a hinge region of an antibody or Ig fusion protein that are involved in heavy chain-heavy chain homodimerization can have significant effects on the expression and assembly of antibodies or Ig fusion

proteins. In particular, a higher number of cysteines can lead to incorrect assembly of an antibody or Ig fusion protein, due to incorrect disulfide bond formation. Thus, the invention discloses that mutation of one or more cysteines involved in heavy chain homodimerization can cause an improvement in expression or assembly of an

5   antibody or Ig fusion protein. In a preferred embodiment, a heavy chain-homodimerization cysteine can be mutated to, in order of general preference, serine, alanine, threonine, proline, glutamic acid, glutamine, lysine, histidine, arginine, asparagine, aspartic acid, glycine, methionine, valine, isoleucine, leucine, tyrosine, phenylalanine, tryptophan or selenocysteine.

10   [0086]   It is particularly convenient to use an IgG1 hinge that is mutated in the first, most N-terminal cysteine. The advantage of this hinge region is that it only has two cysteines. The first cysteine in the IgG1 hinge normally forms a disulfide bond with the a cysteine in the light chain. However, in Ig fusion proteins lacking a light chain, such as Fc-X, X-Fc and X-Fc-Y proteins, the most N-terminal cysteine in the

15   IgG1 hinge serves no such purpose and therefore can be mutated (Lo et al. Protein Engineering 11:405-500 [1998]). As described in the Examples, the two-cysteine IgG1 hinge can also be used in an intact antibody or intact antibody fusion protein in which the CH1 domain derives from IgG2, since the IgG2 CH1 domain has a cysteine that can form a disulfide with the light chain.

20   *Fc Receptors*

[0087]   IgG molecules interact with multiple classes of cellular receptors including three classes of Fcγ receptors (FcγR) specific for the IgG class of antibody, namely FcγRI, FcγRII, and FcγRIII. These receptors are responsible for uptake of antigen-antibody complexes. The Fc receptor binding site on Fc is found on the CH2 domain

25   near the hinge, and it is thought that binding of the V regions to an antigen helps displace the light chain constant region from sterically blocking the hinge. In this way, antibodies bound to antigen are preferentially bound by Fc receptors.

[0088]   A fourth receptor, alternatively termed the 'protection receptor' (FcRp) or the 'neonatal receptor' (FcRn), is responsible for recycling antibodies from the

30   endosome after the endocytosis of antibody-antigen complexes and their disaggregation in the endosome. The binding site for FcRp is found at the junction between the CH2 and CH3 domains in the three-dimensional antibody structure. The

serum nalf-life of IgG antibodies depends on a productive interaction with functional FcRp. Other antibody types, such as IgM, IgD, IgE, and IgA do not bind to FcRp.

[0089]   Another binding partner of certain antibodies is C1q, which mediates complement fixation.

5   [0090]   Interaction with Fc receptors and FcRp also affects the biological activity and metabolism of fusion proteins containing an Fc moiety.

[0091]   For example, fusion proteins with poor binding to FcR have longer serum half-lives than corresponding fusion proteins with good binding to FcR. Fusion proteins with poor binding to FcRp have shorter serum half-lives than corresponding

10   fusion proteins with good binding to FcRp.

[0092]   For example, Ig fusion proteins containing the CH2 and CH3 domains of IgG2 have a longer serum half-life than fusion proteins containing an IgG1. Similarly, fusion proteins containing an Fc region derived from IgG3 have a shorter serum half-life than corresponding fusion proteins containing IgG1 or IgG2. Fusion

15   proteins containing CH2 and CH3 domains derived from IgM, IgD, IgE, and IgA have even shorter serum half-lives than corresponding IgG-derived fusion proteins.

[0093]   To illustrate the uses of the invention, it is convenient to group antibodies and Ig fusion proteins into two general classes: proteins in which immunological effector functions are desired and proteins in which the Ig moiety serves as an

20   immunologically inert carrier and lacks effector functions. In the former category of proteins it is convenient to construct proteins with hybrid isotypes in which a particular constellation of effector functions is created. In the latter category it is convenient to construct proteins with hybrid isotypes involving regions of certain isotypes with minimal effector functions and regions from other isotypes that enhance

25   the assembly of the protein as described below.

Assembly of antibodies and Ig fusion proteins

[0094]   The invention discloses the discovery that the hinge of an antibody or an Ig fusion protein plays a key role in the proper assembly and lack of aggregation of a

30   fusion protein, such as an Ig fusion protein secreted from a mammalian cell. For example, without wishing to be bound by theory, it is thought that antibody and Ig fusion protein assembly involves a step in which two heavy chains first non-

covalently associate by a hydrophobic patch in the CH3 domain. After this association, the hinge regions are aligned and interchain disulfide bonds are formed. The hinge region is about 50 Angstroms from the hydrophobic patch in the CH3 domain.

5   [0095]   In designing an antibody or Ig fusion protein construct, it is useful to vary the hinge region. For example, it is useful to replace the DNA encoding a hinge region in a given expression construct with DNA encoding a different hinge region, such as the hinge region from IgG1, IgG2, IgG3, IgG4, IgM, IgA, IgD, IgE, or IgY.

[0096]   According to a theory of the invention, for example, antibodies and Ig
10   fusion proteins containing hinge regions with a greater number of cysteines do not assemble as efficiently as corresponding proteins with fewer cysteines. Without wishing to be bound by theory, hinge regions with larger number of cysteines exhibit a greater chance for misalignment of the cysteines and incorrect disulfide bond formation. As a result, antibodies and Ig fusion proteins with hinge regions
15   containing a larger number of cysteines are found to be more highly aggregated and exist in multiple electrophoretic species as compared to corresponding antibodies and Ig fusion proteins with hinge regions containing a smaller number of cysteines. Illustrations of this phenomenon are given in the Examples.

[0097]   For example, antibodies and Ig fusion proteins containing a hinge region
20   containing four cysteines are less efficiently assembled than antibodies and Ig fusion proteins containing three or two cysteines. For example, proteins containing an IgG2-derived hinge region are less efficiently assembled than corresponding proteins containing an IgG1-derived hinge region. In a distinct example, proteins containing an IgG3-derived hinge region are poorly assembled; the IgG3 hinge region contains
25   11 cysteines.

[0098]   The utility of the invention is particularly illustrated in situations in which minimal binding to an Fc receptor I is desired. For example, in the context of fusion proteins, it is convenient to use the CH2 and CH3 regions from IgG2 because binding to FcR is profoundly reduced, so that ADCC is reduced and serum half-life is
30   enhanced. However, use of the IgG2 hinge region causes the resultant antibody or Ig fusion to be poorly assembled. It is particularly convenient to use an IgG2 CH2 and

CH3 region in combination with an IgG1 hinge, as illustrated in various Examples below.

[0099]   A parallel finding, illustrated in several Examples, is that the choice of a particular hinge or other domain may affect the production levels of an antibody or Ig fusion. This finding is of great economic importance, since protein drugs such as intact antibodies often need to be dosed in large amounts, such as several hundred milligrams per patient per dose. It is generally found that the choice of a hinge with a minimal number of cysteines, such as three or two, improves the yield of an antibody or Ig fusion protein from a eukaryotic expression system. Lowering the number of cysteines may be accomplished by mutation or by substituting the hinge of one isotype for another, or both.

Enhancement of protease resistance

[0100]   The hinge region is particularly sensitive to proteases. In classical experiments, antibodies were divided into Fab regions and Fc regions by protease cleavage in the hinge region.

[0101]   It is convenient to construct antibodies and Ig fusion proteins with a hinge region from IgA and other components from other antibody isotypes. For example, if an antibody or Ig fusion protein is to be delivered orally or across another mucosal surface such as the nasal, lung, vaginal, or rectal mucosa, it is useful to have a particularly protease-resistant protein to protect the antibody or Ig fusion protein from proteases that are present. For example, it is useful to construct an antibody or Ig fusion protein that contains an IgA hinge and the CH2 and CH3 domains from an IgG, so that this hybrid isotype protein will have the features of protease resistance and an extended serum half-life once the protein enters the circulation. The hinge of IgA1 is a preferred hinge, because the glycosylation sites in the IgA1 hinge confer resistance to a broad spectrum of proteases. In contrast, the hinge of IgA2 is shorter and is resistant to bacterial proteases that specifically cleave the IgA1 hinge.

[0102]   Other isotype heavy chains also contain glycosylation sites that contribute to protease resistance. For example, IgA, IgD, IgE, and IgM contain glycosylation sites in the constant domains that contribute to protease-resistance. For example, the IgE CH1 domain contains three N-linked glycosylation sites. It is useful to combine

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the IgE CH1 domain with, for example, a hinge region from IgA and with CH2 and CH3 domains from an IgG.

[0103]   It is also useful to incorporate glycosylation sites from one isotype into the CH2 or CH3 region of another isotype. In such cases, it is generally not sufficient to construct antibodies or Ig fusion proteins in which entire domains, as defined by regions encoded by single exons, and so it is useful to construct hybrid domains. For example, it is useful to combine the features of FcRp binding characteristic of IgG isotypes and the protease-resistance features of other isotypes. To achieve such a combination of features, it is necessary to construct individual domains with amino acid sequences from two different isotypes. The resulting hybrid domains are then used to construct Ig fusions to non-Ig moieties.

[0104]   For example, it is convenient to substitute a stretch of amino acids from the IgE CH2 domain that include the sequence VNLTW (SEQ ID NO: 3) for the corresponding amino acids in an IgG CH2 domain. For example, in IgG1 these amino acids are VKFNW (SEQ ID NO: 4) and in IgG3 these amino acids are VQFKW (SEQ ID NO: 5). According to the invention, the corresponding amino acids in other CH2 domains can be determined by computer-based or structural alignment of the CH2 domains of other isotypes, or from the published literature (Paul, WE *Fundamental Immunology* Fourth Edition, chapter 3, p. 46-47).

[0105]   Similarly, it is also useful to incorporate other glycosylation sites into IgG. For example, sequence segments that include the NTSGF (SEQ ID NO: 6) or LNASR (SEQ ID NO: 7) sequences from IgD are used to replace the corresponding sequences of an IgG-derived Fc region in an antibody or Ig fusion protein. According to the invention, other useful glycosylation sites within antibody constant regions are disclosed in Paul (*Fundamental Immunology* Fourth Edition, chapter 3) and references therein.

[0106]   In some embodiments of the invention, the incorporation of a non-IgG glycosylation site reduces the interaction with FcRp. In such cases, there is a tradeoff between the improvement in protease resistance and the decrease in serum half-life, and the usefulness of such a hybrid isotype protein must be evaluated in the context of a particular application.

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[0107]   According to the invention, the protease resistance of a particular hybrid isotype antibody or Ig fusion protein is assayed according to standard procedures. Proteases can be purchased from commercial suppliers and are incubated in the presence of a particular hybrid isotype antibody or Ig fusion protein in accordance

5   with the manufacturer's specifications. Proteolysis is measured, for example, by SDS gel electrophoresis and quantitation of starting material and cleavage products.

[0108]   According to the invention, the ability of a hybrid isotype antibody or Ig fusion protein to interact with FcRp is also measured according to standard procedures. For example, the pharmacokinetic properties of an antibody or Ig fusion

10   protein are measured in a mammal such as a mouse, rat, rabbit, dog, non-human primate, or human. The pharmacokinetic properties of an antibody or Ig fusion protein are a practical indication of FcRp binding, and in general, the purpose of incorporating the feature of FcRp binding into an antibody or Ig fusion protein is to improve the pharmacokinetic properties of an antibody. It is also convenient to

15   examine the three-dimensional structure of the FcRp-Fc complex to determine whether a particular hybrid isotype antibody or Ig fusion protein is likely to interact with FcRp (Martin, W. L., et al.: Crystal Structure at 2.8A of an FcRn/Heterodimeric Fc Complex: Mechanism of pH-Dependent Binding. *Mol. Cell* 7 *pp.* 867 [2001]; structure ID 1I1A at http://www.rcsb.org/pdb/).

20   [0109]   According to this aspect of the invention, it is particularly useful to construct proteins of the form Fc-X, wherein the Fc region contains a hinge region from IgA1, a CH2 and CH3 region containing those elements of IgG2 that mediate binding to FcRp, and those elements of CH2 that have reduced effector functions compared to other IgGs.

25

Increasing the valency of an antibody or Ig fusion protein

[0110]   According to the invention, it is sometimes useful to construct a hybrid isotype antibody or Ig fusion protein that has a high valency, but that also has effector functions or other features characteristic of lower-valency antibodies. IgA and IgM

30   have a high valency due to oligomerization via interchain disulfide bonds in the CH3 region. IgA and IgM also have disulfide bonds from a cysteine near the C-terminus of CH4 to the J chain. IgA is dimeric and IgM is pentameric or hexameric, such that IgA has 4 antigen-binding sites and IgM has 10 or 12 antigen-binding sites.

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[0111]   However, IgM and IgA do not mediate ADCC. To construct a polyvalent antibody or Ig fusion that mediates ADCC, it is useful to construct a protein that has the CH2 domain of an IgG and the CH3 and CH4 domains of IgM or IgA. In general, it is preferable to use IgM CH3 and CH4 domains, since the resulting hybrid isotype protein has a higher valency than the corresponding IgA-containing hybrid isotype protein.

[0112]   The following application illustrates the utility of hybrid isotype fusion proteins with increased valency. Many tumor cells overexpress the EGF-receptor on their cell surfaces. The EGF-receptor is also expressed on the surface of many normal cells, so the difference in EGF-receptor expression between normal and tumor cells is only quantitative. According to one embodiment of the invention, a useful IgG-IgM hybrid isotype protein comprises a V region that interacts weakly with the human EGF-receptor. The affinity of the V region is chosen so that the fusion protein does not efficiently interact with EGF-R on normal cells, but interacts with the overexpressed EGF-receptor on tumor cells as a result of an avidity effect. The use of a CH2 domain of an IgG, for example the CH2 domain of IgG1, mediates ADCC against the tumor cells.

[0113]   To enhance the specific killing of tumor cells, it is also useful to fuse the anti-EGF-R IgG-IgM hybrid isotype protein to a protein with anti-tumor activity, such as a cytokine. For example, IL-2 may be used. Alternatively, it is useful to conjugate a radioactive atom to the hybrid isotype protein, such that concentration of the hybrid isotype protein in the region of the tumor causes preferential irradiation of the tumor. For example, Yttrium-90 may be conjugated to the IgG-IgM hybrid isotype protein. The combination of ADCC and IL-2 action or ADCC and irradiation is particularly useful in killing tumor cells.

[0114]   In an IgG-IgM fusion protein, such as the anti-tumor protein described above, it is also generally useful to use a hinge region from IgG, preferably IgG1. The hinge region from IgG3 is, for many applications, the least preferred IgG hinge region, because this hinge region tends to cause variable assembly; moreover, the IgG3 hinge is easily proteolyzed (Baici A, et al., Scand J Immunol. [1980] 12:41-50).

[0115]   The preceding example illustrates a general principle of this aspect of the invention: that an antigen that is more highly expressed on a target cell type than on

normal cells may be more effectively targeted by an antibody or Ig fusion protein with
a high valency but a relatively low monovalent affinity.

[0116]   For example, in autoimmune diseases, certain immune cells such as T cells
express a higher level of cell surface proteins such as cytokine receptors. It is useful
to attack such immune cells with a high valency IgG1, IgG2, or IgG4-IgM antibody or
Ig fusion protein directed against the up-regulated surface protein. In this way,
targeting of cells in which the cell surface protein is present but not up-regulated is
minimized. For example, during an attack of an autoimmune disease, it is useful to
treat a patient with an IgG-IgM fusion protein in which the V regions are directed
against, for example the IL-2 receptor, the IL-12 receptor, or any other up-regulated
receptor. The hinge region and the CH2 domain are preferably derived from IgG1,
IgG2, or IgG4, and the CH3 and CH4 regions are preferably derived from IgM. The
V regions preferably bind weakly to the IL-2 or IL-12 receptor for the treatment of
autoimmune disease. This treatment has the effect of killing a subset of T cells but
not the entire T cell repertoire.

*Construction of expression plasmids that express antibodies and Ig fusion proteins
with hybrid isotypes.*

[0117]   The invention also provides nucleic acids that encode the antibodies and
fusion proteins of the invention. The invention is best practiced when the encoding
nucleic acids also encode a secretion cassette that, when transcribed and translated,
gives rise to a signal peptide. The signal peptide is generally cleaved from the mature
product. The secreted fusion protein can be collected from the culture media without
the need for lysis of the host cell, and can be assayed for activity or purified using
common reagents as desired. In some cases, the presence of certain fusion partners,
such as the cytokine CNTF, allows for secretion of an Ig fusion protein without a
secretion cassette.

[0118]   One of ordinary skill in the art can perform such recombinant DNA
constructions using DNA with introns, because the naturally occuring introns separate
the DNA encoding the hinge from the DNA encoding the CH1 and CH2 domains.
Restriction sites in the introns can be used. Alternatively, because the hinge regions
are generally only about 15 to 70 amino acids long, it is possible to construct synthetic
DNAs encoding an entire hinge region, for example with oligonucleotide synthesis,

PCR, or a combination thereof. The synthetic hinge-encoding region can then be placed into an expression plasmid encoding an Ig fusion protein using standard recombinant DNA techniques.

[0119]   The invention is illustrated further by the following non-limiting examples.

5

EXAMPLES

Example 1: Construction of a plasmid expressing an Fc-X fusion protein with a hinge region and CH2 region from different antibody isotypes.

[0120]   The construction of a plasmid that expresses HuFcγ1-Leptin has been

10   described in the PCT publication WO00/040615A2.

[0121]   A plasmid that expresses a fusion of an IgG2-derived Fc and a C-terminal fusion partner was constructed as follows.

[0122]   First, the genomic sequence of human γ2 Fc was obtained. The genomic DNA encoding human Fcγ2 was obtained by PCR on cellular DNA isolated from

15   human PBMCs. The forward primer had the sequence 5' CC *TTA AGC* GAG CGC AAA TGT TGT GTC GAG (SEQ ID NO: 8), where an AflII restriction site *C TTA AG* was introduced just upstream of the γ2 hinge coding region GAG CGC AAA TGT TGT GTC GAG (SEQ ID NO:9). The reverse primer had the sequence 5' CC*TCGAG* TCA TTT A*CC CGG G*GA CAG GGA G (SEQ ID NO: 10), where an

20   XhoI restriction site *CTCGAG* was introduced immediately after the translation stop codon (anticodon **TCA**). In addition, the reverse primer also introduced a SmaI *CC CGGG* by silent mutation (A to G substitution underlined). The 910 bp PCR fragment was cloned into the TOPO TA Cloning Vector (Invitrogen, Carlsbad, CA) for sequence verification.

25   [0123]   Second, the human γ2 Fc was placed into an expression vector. The natural SmaI restriction site in the DNA sequence CTG CCC CCA T*CC CGG G*AG GAG ATG ACC AAG (SEQ ID NO: 11) encoding the upper CH3 region was deleted by a silent mutation introduced by an overlapping PCR technique (Daugherty, B.L. et al., Nucleic Acids Res. 19:2471-6, 1991). The forward prim_ had the sequence 5'

30   CTG CCC CCA TC<u>A</u> CGG GAG GAG ATG ACC AAG (SEQ ID NO: 12), where the C to A substitution is underlined; and the reverse primer had the sequence 5' GGT CAT CTC CTC CCG <u>T</u>GATGG GGG CAG GGT GTA C (SEQ ID NO: 13), where

the G to T substitution is underlined. After sequence verification, the resultant AflII-

XhoI restriction fragment encoding the Fc of γ2 contained a unique SmaI site

upstream of the translation stop codon, and a XhoI site downstream of the stop codon.

The AflII-SmaI fragment encoding Fcγ2 was then used to replace the corresponding

5   restriction fragment encoding Fcγ1 in pdCs-huFcγ1-Leptin (PCT publication

WO00/040615A2) to give pdCs-huFcγ2-Leptin.

[0124]   Third, the DNA encoding the hinge of the Fc γ2 was replaced by the

altered hinge from γ1. The γ2 hinge region contains four cysteine disulphide bonds.

Shown below is the AflII-StuI fragment containing the γ2 hinge exon. The AflII site

10   (C TTA AG) is preceded by DNA sequence encoding a signal peptide. Glutamic acid

(E) is the first amino acid residue of the γ2 hinge. The letters in small case represent

the intron sequence following the γ2 hinge exon. The StuI restriction site (aggcct) is

C-methylated in most E. coli strains by the DCM methylase because of the C-

methylation in the sequence ccagg and the reverse strand cctgg; when methylated, this

15   site cannot be cut by StuI.

              E   R   K   C   C   V   E   C   P   P   C   P (SEQ ID NO:

     14)

     C TTA AGC GAG CGC AAA TGT TGT GTC GAG TGC CCA CCG TGC CCA G

20   gtaagccagcccaggcct (SEQ ID NO: 15)

     [0125]   The AflII-StuI fragment containing the γ2 hinge exon in pdCs-huFcγ2-

     Leptin was replaced by the corresponding AflII-StuI fragment containing the γ1 hinge

     exon from pdCs-huFc γ1-Leptin, which is shown below:

25

              E   P   K   S   S   D   K   T   H   T   C   P   P   C   P (SEQ ID NO:

     16)

     C TTA AGC GAG CCC AAA TCT TCT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA G

30   Gtaagccagcccaggcct (SEQ ID NO: 17)

                                          28

[0126]   The γ1 hinge sequence in pdCs-huFc γ1 contains a Cys to Ser mutation (underlined) which eliminates the Cys residue that forms a disulphide bond with the light chain in IgG1 (Lo et al., (1998) Protein Engineering 11:495-500). Since the StuI sites in both the γ1 and γ2 exons are C-methylated and the StuI restriction

5   endonuclease is methylation sensitive, both plasmids were isolated from a DCM negative strain of bacteria before digestion with the StuI enzyme. The resultant pdCs-huFcγ2-Leptin with the hinge region from pdCs-huFc γ1 was designated pdCs-huFcγ2h-Leptin (γ2h: γ2 with altered hinge).

10   **Example 2: Characterization of the oligomerization state of huFc γ2-leptin and huFcγ2h-leptin immunofusion.**

[0127]   Protein expression from NS/0 cells using expression vector pdCs-huFc-huLeptin with the γ1, γ2, and γ2h isotypes was evaluated. The physical state of different forms of huFc-huLeptin in which the huFc moiety derived from γ1, γ2, and

15   γ2h isotypes were evaluated.

[0128]   DNA constructs generated as described above and as in Lo et al. were transfected into NS/0 cells and stable expressing cell lines were generated according to standard procedures.

[0129]   In this and the following Examples, stable transfectants were generated as

20   follows. Plasmid DNAs were introduced into the mouse myeloma NS/0 cells by electroporation. NS/0 cells were grown in Dulbecco's modified Eagle's medium supplemented with 10% fetal bovine serum, 2 mM glutamine and penicillin/streptomycin. About 5×10^6 cells were washed once with PBS and resuspended in 0.5 ml PBS. Ten μg of linearized plasmid DNA were then incubated

25   with the cells in a Gene Pulser Cuvette (0.4 cm electrode gap, BioRad) on ice for 10 min. Electroporation was performed using a Gene Pulser (BioRad, Hercules, CA) with settings at 0.25 V and 500 μF. Cells were allowed to recover for 10 min. on ice, after which they were resuspended in growth medium and then plated onto two 96 well plates. Stably transfected clones were selected by growth in the presence of 100

30   nM methotrexate (MTX), which was introduced two days post-transfection. The cells were fed every 3 days for two to three more times, and MTX-resistant clones appeared in 2 to 3 weeks. Supernatants from clones were assayed by anti-Fc ELISA

to identify high producers. High producing clones were isolated and propagated in growth medium containing 100 nM MTX.

[0130]   Concentration of HuFc-huLeptins in the supernatant was determined by an anti-huFc ELISA, using anti-huFc antibody (horseradish peroxidase-conjugated goat

5   anti-huIgG, Fcγ1 or Fcγ2, from Jackson ImmunoResearch). Relatively low levels of expression were detected in the supernatants of the γ2 constructs whereas the γ1 and γ2h constructs gave high levels of expression in both transient and stable transfections. In transient transfections with equivalent expression vectors encoding huFcγ2-huLeptin and huFcγ2h-huLeptin, the huFcγ2h-huLeptin was produced at 8-

10   fold higher levels.

[0131]   For purification, the fusion proteins in tissue culture supernatants were bound to Protein A Sepharose followed by elution in a sodium phosphate buffer (100 mM NaH_2PO_4, pH 3, and 150 mM NaCl). The eluate was then neutralized with 0.1 volume of 2 M Tris-hydrochloride, pH 8 and evaluated by SDS-polyacrylamide gel

15   electrophoresis (SDS-PAGE) and HPLC - size exclusion chromatography (SEC).

[0132]   Fusion proteins were examined by SDS-PAGE under non-reducing conditions. The protein bands, visualized by Coomassie staining, showed HuFcγ1-huLeptin to have an apparent MW of 96 kD, indicating a bivalent monomer. Analysis by SDS-PAGE showed that much of the huFcγ2-huLeptin fusion protein was in a

20   higher molecular weight form, migrating as a ladder of bands with apparent molecular weights much higher than Fc-Leptin. In contrast, huFcγ2h-huLeptin was primarily a single species, migrating at 96 kD.

[0133]   Size exclusion chromatography (SEC) analysis of huFcγ2h construct correlated with SDS-PAGE results and showed both huFcγ2h-leptin and huFcγ1-

25   leptin to be about 83% monomeric, while the comparable huFcγ2-huLeptin fusion protein was about 55 % monomeric.

[0134]   Studies with fixed J774 cells, which are rich in the FcγR class of receptors, showed that only the huFcγ1-huLeptin fusion protein exhibits Fc binding. In addition, BAF-3 cells transfected to express the leptin receptor so that their proliferation could

30   be stimulated by leptin (Gainsford, T., et al. PNAS [1996] 93:14564-14568) were

used. Studies with BAF3/leptin receptor cells showed that huFcγ1-huLeptin, huFcγ2-huLeptin and huFcγ2h-huLeptin were equivalent in leptin bioactivity.

[0135]   Stable clones of mammalian cells expressing huFcγ2-huLeptin and huFcγ2h-huLeptin were also identified. Cell transfections were carried out under essentially identical conditions and an identical number of stably transfected cells were cloned and tested for production of huFcγ2-huLeptin and huFcγ2h-huLeptin. The best-expressing clone for huFcγ2h-huLeptin made about 5-fold more huFc-huLeptin than the best-expressing clone for huFcγ2-huLeptin.

Example 3: Construction of a plasmid expressing an X-Fc fusion protein with a hinge region and CH2 region from different antibody isotypes.

[0136]   The synthetic DNA sequence (SEQ ID NO: 18) encoding glucagon-like peptide 1 (GLP-1) amino acid residues 7 to 37 (SEQ ID NO: 19) is disclosed below.

        H   A   E   G   T   F   T   S   D   V   S   S   Y   L   E   G
C TTA AGC CAT GCT GAA GGG ACC TTT ACT AGT GAT GTA AGT TCT TAT TTG GAA GGC

        Q   A   A   K   E   F   I   A   W   L   V   K   G   R   G
CAA GCT GCC AAG GAA TTC ATT GCT TGG CTG GTG AAA GGC CGA GGA *GGA TCC TTA*

AGC

[0137]   The DNA encoding the GLP-1 peptide was preceded by *C TTA AGC*, where the AflII restriction site was used to join this DNA fragment to the DNA fragment encoding the signal sequence (Lo et al. Protein Engineering). At the 3' end, the DNA encoding GLP-1 was followed by a BamHI restriction site (*GGA TCC*, which encodes the amino acid residues G and S), and an AflII restriction site, which was used to ligate to the AflII-XhoI restriction fragment encoding Fc γ 2 (or Fc γ 2h) with a translation stop codon (see Example 1).

Example 4: Characterization of the oligomerization state of GLP1-huFc γ2 and GLP1-huFc γ2h immunofusions.

[0138]   The resultant vectors from Example 3, pdCs GLP-1 huFcγ1, pdCs GLP-1 huFcγ2, and pdCs GLP-1 huFcγ2h, were used to transiently and stably transfect

mammalian cells for the expression of GLP-1 (7-37) huFc γ1, GLP-1 (7-37) huFc γ2 and GLP-1 (7-37) huFc γ2h.

[0139]   Assessment of aggregation state and total protein expression for each GLP-1 huFc fusion protein was performed by SDS-PAGE and HPLC-SEC after

5   purification by Protein A Sepharose, using the general methods described in Example 2. The protein bands were visualized by Coomassie staining. GLP-1 huFcγ2 and GLP-1 huFcγ2h had an apparent MW of approximately 60 kD by SDS-PAGE. Concentration of GLP-1 huFc variants in the supernatant was determined by anti-huFc ELISA. In transient transfections with equivalent expression vectors encoding

10   GLP1-huFcγ2 and GLP1-huFcγ2h, the GLP1-huFcγ2h was produced at about 1.5-fold higher levels.

[0140]   Analysis of total cell lysates by SDS-PAGE showed that about half of the GLP1-huFcγ2 fusion protein had incorrect disulfide bonds, as illustrated by the presence of several high molecular weight forms migrating with an apparent weight of

15   100 to 200 kD. In contrast, essentially all of the detectable GLP1-huFcγ2h fusion protein migrated with an apparent molecular weight of about 60 kD. When the samples were reduced before SDS-PAGE, the GLP1-huFcγ2 and GLP1-huFcγ2h proteins ran with an essentially identical apparent molecular weight of about 34 kD.

[0141]   Comparative analysis by HPLC-SEC of the γ1, γ2 and γ2h fusion proteins

20   demonstrated that the modified γ2h fusion protein was significantly more monomeric than the other fusion proteins. The modified GLP1-huFcγ2h fusion protein, as illustrated by a single peak, was 84% bivalent monomer, while both the GLP1-huFcγ1 and GLP1-huFcγ2 fusions proteins had multiple peaks corresponding to approximately 42 and 33% bivalent monomer, respectively.

25   [0142]   Thus, the GLP-1-Fc fusion protein bearing the hinge of IgG1 and the CH2 and CH3 domains of IgG2 showed surprisingly better assembly properties than GLP-1-Fc fusion proteins in which the entire Fc region derived from either IgG1 or IgG2.

Example 5: Construction of an intact antibody specific for diseased cells that
contains IgG2 CH1, CH2, and CH3 domains and an IgG1 hinge.

[0143]   The genomic DNA encoding the immunoglobulin γ 2 constant regions
(CH1, hinge, CH2 and CH3) was obtained by PCR using cellular DNA isolated from
5   human PBMCs. The forward primer had the sequence 5' C*A*
*AGCTTT*CTGGGGCGAGC (SEQ ID NO: 20), where a HindIII restriction site *A*
AGCTT was introduced to the intron sequence about 220 bp upstream of the CH1
exon. The reverse primer has the sequence 5' C*CTCGAG* TCA TTT A*CC CGG*
*G*GA CAG GGA G (SEQ ID NO: 21), where an XhoI restriction site *CTCGAG* was
10   introduced immediately after the translation stop codon (anticodon **TCA**), and a SmaI
CC CGGG was created by silent mutation, as already described in Example 1. The
natural SmaI restriction site in the DNA sequence encoding the upper CH3 region was
also deleted by a silent mutation introduced by overlapping PCR, as described in
Example 1. One skilled in the art would also recognize that by taking advantage of
15   restriction fragments encoding the Fcγ2 obtained in Example 1, a ~1810 base pair (bp)
HindIII-XhoI restriction fragment encoding the CH1, hinge, CH2 and CH3 regions
and containing a unique SmaI restriction site could be readily constructed. After
sequence verification, the HindIII-XhoI fragment encoding γ2 constant regions was
used to replace the HindIII-XhoI fragment encoding γ1 constant regions-IL2 in
20   pdHL7-huKSγ1-IL2 to give pdHL7-huKSγ2 antibody.

[0144]   The expression vector for huKSγ2h antibody was constructed as follows.
The plasmid pdCs-huFcγ2h-Leptin was used as the PCR template for creating a ~130
bp PstI-PvuII restriction fragment encoding the cysteine-to-serine modified γ1 hinge
region only. The forward primer had the sequence 5' *CTGCAG*AGCCCAAATCTTC
25   (SEQ ID NO: 22), which restored the native PstI (*CTGCAG*) restriction site at the
beginning of the γ1 hinge exon (with the C to S mutation described above). The
reverse primer had the sequence 5' *CAGCTG*GGGGCCTGTCCCTG (SEQ ID NO: 23),
which corresponded to the PvuII site (*CAGCTG*) in the intron between the hinge and
the CH2 exons. After sequence verification, this ~130 bp PstI-PvuII restriction
30   fragment was used to replace the corresponding fragment in pdHL7- huKSγ2 antibody
to give the pdHL7-huKSγ2h antibody.

Example 6: Characterization of the non-reduced state of a γ2-antibody and a corresponding γ2h antibody directed against diseased cells.

[0145]   For transient transfection, the vectors, pdHL7 of KS antibody with IgGγ1, γ2, and γ2h isotypes were introduced into mammalian cells by lipofection using Lipofectamine Plus (Life Technologies, Gaithersburg, MD) according to supplier's protocol. Stable transfectants were generated as described in Example 2.

[0146]   KS antibodies in the conditioned media (10% serum) were captured on Protein A Sepharose (Repligen, Cambridge, MA) and then eluted by boiling in the protein sample buffer with or without 2-mercaptoethanol prior to characterization by SDS-PAGE. Visualization by Coomassie staining showed non-reduced KS γ2 antibody to migrate as several species with molecular weights of approximately 150 kD. In contrast, the KSγ2h antibody migrated as a major band with an apparent molecular weight of 150 kD. When the KS γ2 antibody and KS γ2h antibody were reduced with mercaptoethanol before SDS-PAGE, an identical pattern of bands corresponding to the heavy and light chains was observed for both the KSγ2 antibody and KSγ2h antibody.

[0147]   Without wishing to be bound by theory, these observations suggest that the distinctly migrating species seen with KSγ2 were due to variations in disulfide bonding patterns.

[0148]   Stable clones of mammalian cells expressing KSγ2 antibody and KSγ2h antibody were also identified. Cell transfections were carried out under essentially identical conditions and similar numbers of stably transfected cells were cloned and tested for production of huFc KSγ2 antibody and KSγ2h antibody. The four best-expressing clones for KSγ2h antibody made about 114, 98, 85, and 49 micrograms of antibody per ml of tissue culture supernatant, while under the same conditions the four best-expressing clones for huFc KSγ2 antibody made about 36, 34, 15, and 13 micrograms of antibody per ml of tissue culture supernatant.

Example 7: Construction of a fusion protein including a complete antibody that contains IgG2 CH1, CH2, and CH3 domains and an IgG1 hinge.

[0149]   In this Example, the usefulness of an antibody fusion protein in which the antibody moiety had a hybrid isotype was examined.

[0150]   The expression vector for huKSγ2-IL2, pdHL7-huKSγ2-IL2, was constructed by replacing the SmaI-XhoI restriction fragment in pdHL7-huKSγ2 antibody, which contains the sequence GGGTAAATGA (SEQ ID NO: 24) followed by the XhoI sticky end, by the SmaI-XhoI restriction fragment isolated from pdHL7-huKS-IL2. This latter fragment contains the sequence GGGTAAA followed immediately by the DNA sequence encoding the mature IL2 including the translation stop codon. The resultant expression vector, pdHL7-huKSγ2-IL2, was used to transfect cells for protein expression.

[0151]   Similarly, the expression vector for huKSγ2h-IL2, pdHL7-huKSγ2h-IL2, was constructed by replacing the SmaI-XhoI restriction fragment in pdHL7-huKSγ2h antibody, which contains the sequence GGGTAAATGA (SEQ ID NO: 24) followed by the XhoI sticky end, by the SmaI-XhoI restriction fragment isolated from pdHL7-huKS-IL2 as described in the preceding paragraph. The resultant expression vector, pdHL7-huKSγ2h-IL2, was used to transfect cells for protein expression.

Example 8: Characterization of the non-reduced state of a γ2-antibody fusion protein and a corresponding γ2h antibody fusion protein.

[0152]   For transient transfection, the plasmids encoding KS γ2-IL2 and KS γ2h-IL2 were introduced into mammalian cells by lipofection using Lipofectamine Plus (Life Technologies, Gaithersburg, MD) according to supplier's protocol.

[0153]   In order to obtain stably transfected clones, plasmid DNAs were introduced into mouse myeloma NS/0 cells by electroporation as described in Example 2.

[0154]   KS-IL2 fusion proteins with the γ2 and γ2h isotypes were characterized by SDS-PAGE as described in Example 6. Antibody fusion proteins in the conditioned media (10% serum) were captured on Protein A Sepharose (Repligen, Cambridge, MA) and then eluted by boiling in the protein sample buffer with or without 2-mercaptoethanol prior to characterization by SDS-PAGE. Visualization by Coomassie staining showed non-reduced KSγ2-IL2 to migrate as several species with molecular weights of approximately 180 kD. In contrast, the KSγ2h-IL2 migrated as a major band with an apparent molecular weight of about 180 kD. When the KSγ2-

IL2 and KSγ2h-IL2 were reduced with mercaptoethanol before SDS-PAGE, an identical pattern of bands corresponding to the heavy chain-IL2 and light chains was observed for both the KSγ2-IL2 and KSγ2h-IL2.

[0155]   Without wishing to be bound by theory, these observations suggest that the distinctly migrating species seen with KSγ2-IL2 were due to variations in disulfide bonding patterns.

[0156]   The modified γ2h immunocytokines are tested in animals and have extended half-lives with better efficacy in animal tumor models relative to original IgGγ1-based immunocytokines.

[0157]   Stable clones of mammalian cells expressing KSγ2-IL2 and KSγ2h-IL2 were also identified. Cell transfections were carried out under essentially identical conditions and similar numbers of stably transfected cells were cloned and tested for production of KSγ2-IL2 and KSγ2h-IL2. The four best-expressing clones for KSγ2h-IL2 made about 52, 37, 31, and 30 micrograms of fusion protein per ml of tissue culture supernatant, while under the same conditions the four best-expressing clones for KSγ2-IL2 made about 31, 27, 27, and 17 micrograms of fusion protein per ml of tissue culture supernatant.

Example 9: Construction of plasmids expressing antibody fusion proteins with a hybrid isotype and a secondary mutation affecting fusion protein activity.

HuKSγ2-Ala-IL2 vs huKSγ2h-Ala-IL2

[0158]   The expression vectors pdHL7-huKSγ2-Ala-IL2 and pdHL7-huKSγ2h-Ala-IL2 (described above) were constructed by replacing the SmaI-XhoI restriction fragment in pdHL7-huKSγ2 antibody and pdHL7-huKSγ2h antibody, respectively, which contains the sequence GGGTAAATGA (SEQ ID NO: 24) followed by the XhoI sticky end, by the corresponding SmaI-XhoI restriction fragment isolated from pdHL7-huKSγ1-Ala-IL2. This latter fragment contains the sequence GGGTGCA followed immediately by the DNA sequence encoding the mature IL2 including the translation stop codon. The GCA encodes the lysine to alanine substitution at the junction of the fusion protein. The resultant vectors were used to transfect cells for the production of huKSγ2-Ala-IL2 and huKSγ2h-Ala-IL2.

Example 10: Characterization of the non-reduced state of a γ2-antibody fusion protein and a corresponding γ2h antibody fusion protein carrying a secondary mutation affecting fusion protein function.

5   [0159]   For transient transfection, the plasmids encoding KSγ2-Ala-IL2 and KSγ γ2h-Ala-IL2 were introduced into mammalian cells by lipofection using Lipofectamine Plus (Life Technologies, Gaithersburg, MD) according to supplier's protocol.

[0160]   Stable clones of mammalian cells expressing KSγ2-Ala-IL2 and KSγ2h-
10   Ala-IL2 were also identified as in Example 2. Cell transfections were carried out under essentially identical conditions and similar numbers of stably transfected cells were cloned and tested for production of KSγ2-Ala-IL2 and KSγ2h-Ala-IL2. The three best-expressing clones for KSγ2h-Ala-IL2 made about 39, 38, and 29 micrograms of fusion protein per ml of tissue culture supernatant, while under the
15   same conditions the three best-expressing clones for KSγ2-Ala-IL2 made about 22, 17, and 6 micrograms of fusion protein per ml of tissue culture supernatant. KS-Ala-IL2 fusion proteins with the γ2 and γ2h isotypes were characterized by SDS-PAGE as described in Example 6. KS-Ala-IL2 fusion proteins in the conditioned media (10% serum) were captured on Protein A Sepharose (Repligen, Cambridge, MA) and then
20   eluted by boiling in the protein sample buffer with or without 2-mercaptoethanol prior to characterization by SDS-PAGE. Visualization by Coomassie staining showed non-reduced KSγ2-Ala-IL2 to migrate as several species. In contrast, the KSγ2h-Ala-IL2 migrated as one major species. When the KSγ2-Ala-IL2 and KSγ2h-Ala-IL2 are reduced with mercaptoethanol before SDS-PAGE, an identical pattern of bands
25   corresponding to the heavy chain-IL2 and light chains was observed for both the KSγ2-Ala-IL2 and KSγ2h-Ala-IL2.

[0161]   Without wishing to be bound by theory, these observations suggest that the distinctly migrating species seen with KSγ2-Ala-IL2 were due to variations in disulfide bonding patterns.

30

Example 11: Expression of an antibody fusion protein with constant regions derived from different isotypes.

[0162]   In some cases, it is desirable to construct an Ig fusion protein in which different constant regions, in addition to the hinge region, are derived from different

5   heavy chain isotypes. To examine the properties of this class of molecules, the following experiments were conducted.

[0163]   The huKS(γ1:CH1-H)(γ2:CH2-CH3)-Ala-IL2 protein, which is an antibody-IL2 fusion protein with the IgG heavy chain comprising the KS VH, the CH1 and hinge regions from IgG1 and CH2-CH3 regions from IgG2 (with the lysine

10   to alanine substitution at the fusion junction, as described above) followed by IL-2, was expressed as follows. The expression vector pdHL7-huKS(γ1:CH1-H)(γ 2:CH2-CH3)-Ala-IL2 was constructed by replacing the HindIII-AflIII restriction fragment in pdHL7-KS γ2-Ala-IL2 with the corresponding HindIII-AflIII restriction fragment containing the CH1 and hinge regions from pdHL7-KS-IL2. This expression vector

15   was transfected into cultured mammalian cells as described above to yield an antibody fusion protein with a hybrid isotype.

[0164]   The HuKS(γ1:CH1-H)(γ2:CH2-CH3)(Ala)-IL2 hybrid and HuKSγ2(Ala)-IL2 antibody-cytokine fusion proteins were characterized by non-reducing SDS-PAGE as described in Example 6. The HuKS(γ1:CH1-H)(γ2:CH2-CH3)(Ala)-IL2

20   hybrid isotype fusion protein migrated as a major band with a molecular weight of about 180kD. In contrast, the HuKSγ2(Ala)-IL2 antibody-cytokine fusion protein migrated as multiple bands in the 180 kD size range.

[0165]   When the HuKS(γ1:CH1-H)(γ2:CH2-CH3)(Ala)-IL2 hybrid and HuKS(γ2)(Ala)-IL2 antibody-cytokine fusion proteins were characterized by reducing

25   SDS-PAGE, both proteins gave an identical pattern of bands, corresponding to the light chain and the heavy chain-IL2 fusion polypeptides.

[0166]   Without wishing to be bound by theory, it appeared that the HuKS(γ2)(Ala)-IL2 antibody-cytokine fusion protein existed in at least two different isomeric configurations, in which the difference was due to a difference in disulfide

30   bonding pattern.

Example 12: Expression of hybrid isotype antibody fusion proteins with a non-
protein antigen specificity and a multi-subunit fusion partner.

[0167]   The 14.18 antibody binds to the glycolipid antigen GD2. Interleukin-12 is
a heterodimeric cytokine that includes a p35 and p40 subunit, covalently attached by a
5   disulfide bond.

[0168]   As described above, use of a hybrid isotype, such as an IgG1/IgG2 hybrid,
leads to enhanced assembly as compared to a natural isotype, such as IgG2.
Enhanced assembly may be evidenced by increased expression levels.

[0169]   In one case, 14.18(γ2)-Ala-IL12 and 14.18(γ2h)-Ala-IL12 expression
10   plasmids were constructed and transiently transfected into cells in parallel under
identical conditions as described above and in Gillies et al. (WO09929732). Human
IL-12 was used. The level of protein in the tissue culture supernatant was about 40%
higher from the cultures transfected with the 14.18(γ2h)-Ala-IL12 expression plasmid
than from the cultures transfected with the 14.18(γ2)-Ala-IL12 expression plasmid.

15   [0170]   The 14.18(γ2)-Ala-IL12 and 14.18(γ2h)-Ala-IL12 expression plasmids
were also stably transfected into cells as described above, and the four highest-
expressing clones from each transfection were studied further. For 14.18(γ2h)-Ala-
IL12, the average of the four best-expressing clones was about 45% higher than for
the four best-expressing clones derived from the 14.18(γ2)-Ala-IL12 expression
20   plasmid.

[0171]   In a second case, 14.18(γ2)-IL12 and 14.18(γ2h)-IL12 expression plasmids
were constructed and transiently transfected into cells in parallel under identical
conditions as described above. Mouse IL-12 was used. The level of protein in the
tissue culture supernatant was about 40% higher from the cultures transfected with the
25   14.18(γ2h)-IL12 expression plasmid than from the cultures transfected with the
14.18(γ2)-IL12 expression plasmid.

[0172]   The 14.18(γ2)- IL12 and 14.18(γ2h)- IL12 expression plasmids using
murine IL-12 were also stably transfected into cells as described above, and the four
highest-expressing clones from each transfection were studied further. For
30   14.18(γ2h)-IL12, the average of the four best-expressing clones was about 35% higher
than for the four best-expressing clones derived from the 14.18(γ2)-IL12 expression

plasmid.

[0173]   These results indicated that use of a hybrid isotype in a fusion protein led
to enhanced expression, even when using a different antibody and different non-Ig
moiety than in the previous examples. In this Example, the use of IL-12 as the non-Ig
moiety is expected to significantly complicate the assembly of the Ig fusion protein,
because IL-12 is a heterodimer. Nonetheless, the use of a hybrid isotype had a
beneficial effect.

Example 13: Expression of hybrid isotype antibody fusion proteins using a hinge
region from IgA.

[0174]   To construct an Ig fusion protein with enhanced protease resistance, an
IgA/IgG fusion protein is produced.

[0175]   For example, an Fc-X fusion protein is constructed that contains the hinge
region of human IgA1 and the CH2 and CH3 regions of IgG2.

[0176]   An example of the construction of an expression vector to produces an Fc-
X fusion protein comprising the hinge region from human IgA1 and the CH2 and
CH3 regions of IgG2 is as follows. The plasmid pdCs-huFcγ2-Leptin from Example
1 is used as a vector.

[0177]   The AflII-StuI fragment containing the γ2 hinge exon in pdCs-huFcγ2-
Leptin is replaced by the corresponding AflII-StuI fragment (SEQ ID NO: 25)
containing the IgA1 hinge exon, which is shown below:

```
(AflII)    P    S    T    P    P    T    P    S    P    S    T    P
CTTAAG T  CCC  TCA  ACT  CCA  CCT  ACC  CCA  TCT  CCC  TCA  ACT  CCA


P    T    P    S    P    S    C    C    H   (SEQ ID NO:26) (StuI)
CCT  ACC  CCA  TCT  CCC  TCA  TGC  TGC  CAC  Ggtaagccagcccaggcct
```

[0178]   Specifically, the following oligonucleotides are synthesized:

Top strand:

5'-

TTAAGTCCCTCAACTCCACCTACCCCATCTCCCTCAACTCCACCTACCCCATCTCCC

5   TCATGCTGCCACGGTAAGCCAGCCCAGG-3' (SEQ ID NO: 27)

Bottom strand:

5'-

CCTGGGCTGGCTTACCGTGGCAGCATGAGGGAGATGGGGTAGGTGGAGTTGAGGGAGA

10   TGGGGTAGGTGGAGTTGAGGGAC-3' (SEQ ID NO: 28)

[0179]   These oligonucleotides are annealed, and used to replace the
corresponding fragment in pdCs-huFcγ2-Leptin.

[0180]   Since the StuI sites in the γ2 exon is C-methylated and the StuI restriction
15   endonuclease is methylation sensitive, the plasmid is isolated from a DCM negative
strain of bacteria before digestion with the StuI enzyme. The resultant pdCs-huFcγ2-
Leptin with the hinge region from IgA1 is designated pdCs-huFcα1/γ2-Leptin.

[0181]   The plasmid pdCs-huFcα1/γ2-Leptin is transfected into eukaryotic cells
and an Fc-X protein of the form α1(hinge)-γ2(CH2, CH3)-leptin is expressed as a
20   secreted protein. For example, the cells and methods of Example 2 are used. The
resulting α1-γ2-leptin protein is purified, characterized, and found to possess leptin
activity and to be relatively insensitive to protease cleavage in the hinge region.

Example 14: Expression of hybrid isotype antibody fusion proteins using
components of IgG and a polyvalent immunoglobulin.

25   [0182]   To construct antibody fusion proteins with the effector functions of an
IgG, such as IgG1 or IgG3, and an increased valency, a hybrid isotype Ig fusion
protein using the CH1, hinge, and CH2 regions of an IgG and the CH3 and CH4
regions of an IgA or IgM are constructed. Figure 4 shows the structure of an IgG-
IgM hybrid isotype fusion antibody. It is convenient to fuse a non-Ig moiety to the C-
30   terminus of the IgA or IgM CH4 domain.

[0183]   It is also convenient to truncate the IgA or IgM heavy chain before the
most C-terminal cysteine, or to mutate this cysteine, especially when the IgG/IgA or

IgG/IgM hybrid isotype fusion protein is expressed in the absence of a J chain. The normal function of this C-terminal cysteine is to form a disulfide bond with the J chain. It is often desirable to express an IgG/IgA or IgG/IgM hybrid isotype fusion protein in the absence of a co-expressed J chain, especially when fusing the non-Ig

5   moiety to the C-terminus of the heavy chain.

[0184]   For example, an IgG-IgM hybrid isotype fusion protein is constructed as follows. The plasmid pdHL7-huKSγ1-IL2 is capable of expressing an antibody with variable regions that bind to Epithelial Cell Adhesion Molecule and constant regions from human IgG1. This plasmid contains a unique Ngo M IV site in the intron

10   between the IgG1 CH2 and CH3 coding sequences, and also contains a unique XmaI site at the junction between the coding sequences for the IgG1 CH3 and the IL-2 moieties. A DNA fragment encoding the human IgM CH3 and CH4 sequences is generated by PCR amplification from human genomic DNA using the following primers:

15

5'-GCA *GCCGGC* CCTGAGCCTTGGCTTCCCAGAGCG-3' (SEQ ID NO: 29); and
5'- GCT *CCCGGG* <u>TCA</u>GTAGCAGGTGCCAGCTGTGTCG-3' (SEQ ID NO: 30)

20

[0185]   Alternatively, the following primers are used; these have the feature that the C-terminal-most cysteine in the IgM moiety is mutated to a serine.

5'-GCA *GCCGGC* CCTGAGCCTTGGCTTCCCAGAGCG-3'; (SEQ ID NO:
25   31) and
5'- GCT *CCCGGG* <u>TCA</u>GTAGCTGGTGCCAGCTGTGTCG-3'(SEQ ID NO: 32);

[0186]   The resulting DNA fragment is cleaved with Ngo M IV and XmaI and is then directly or indirectly ligated to pdHL7-huKSγ1-IL2 that has been cut with Ngo

30   M IV and XmaI. For example, the PCR fragment encoding the IgM CH3 and CH4 domains is first subcloned into a vector such as the TA cloning vector (Invitrogen, Carlsbad CA), the sequence of the insert is verified, and then the insert is removed using Ngo M IV and XmaI and ligated into pdHL7-huKSγ1-IL2. The amino acid

sequence of a resulting hybrid isotype heavy chain, fused to human IL-2 is shown in
SEQ ID 33. The IgM portion of the fusion protein is underlined. Because of naturally
occuring polymorphisms in human IgM heavy chains, it is also possible to generate
closely related sequences that are functionally similar.

5

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
10   YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKDQDTAIRVFAIPPSFAS
IFLTKSTKLTCLVTDLTTYDSVTISWTRQNGEAVKTHTNI
SESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSP
LKQTISRPKGVALHRPDVYLLPPAREQLNLRESATITCLV
15   TGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYF
AHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKST
GKPTLYNVSLVMSDTAGTCY

(SEQ ID NO:33)
20

[0187]   Many alternative DNA construction strategies are possible. For example,
a DNA sequence encoding the IgM CH3 and CH4 domains may be generated by RT-
PCR from an IgM-expressing cell line or cell population. The 3' PCR primer may be
identical to that shown above, but the 5' primer incorporates an artificial 5' splice site
25   between the Ngo M IV site and the beginning of the IgM CH3 coding sequence.

[0188]   Eukaryotic cells are then transformed with the resulting plasmid, pdHL7-
huKSγ1/μ-IL2, and the resulting protein is expressed and secreted from the cells. For
example, the cells and methods described in the previous Examples are used. The
purified protein is tested, for example by electron microscopy or by size-exclusion
30   chromatography, and found to have a multimeric structure. The purified protein is
further studied, for example by peptide mapping, and it is found that the cysteine in
the sequence ...ASICEDD.... (SEQ ID NO: 34) forms an interchain disulfide bond
with other IgG/IgM hybrid isotype subunits. An example of such a linkage is
illustrated in Figure 4. In addition to the pentameric structure of Figure 4, the final
35   form of the IgG/IgM hybrid isotype protein may be hexameric or some other type of
multimeric structure.

[0189]   The resulting IgG/IgM hybrid isotype fusion protein is found to bind to

43

Fcγ receptors. For example, the fusion protein binds to J774 cells in a manner that is competitive with human IgG.

Example 15: Expression of hybrid isotype antibody using components of IgG1 and IgG4.

5   **[0190]**   The purpose of the experiments in Examples 15-17 was, in part, to demonstrate the utility of hybrid isotype antibodies in improving the assembly of molecules consisting primarily of IgG4. In general, a commonly preferred form of an IgG molecule is the H_2L_2 form, with two heavy chains and two light chains. However, a significant fraction of IgG4 antibodies are synthesized as HL "half

10   molecules" with one heavy chain and one light chain. Angal et al. (1993; Molec. Immunol. 30:105) described a serine to proline substitution that decreased the amount of "half molecules" found in secreted human IgG4.

[0191]   This example compares the assembly properties of three antibodies containing the same V regions: an IgG4 form, a form with a hinge from IgG1 and the

15   CH1, CH2, and CH3 domains from IgG4, and an IgG4 form with a mutation in the hinge region (Angal et al., ibid.).

[0192]   Using standard plasmid construction techniques, a plasmid termed pdHL7-KS-γ4 was constructed. This plasmid is identical to the plasmid pdHL7-huKSγ2 described in Example 5, except that it encodes an IgG4 heavy chain constant region

20   instead of an IgG2 heavy chain constant region.

[0193]   To construct pdHL7- KS-γ4h, the pdHL7-KS-γ2h plasmid was grown in a *dcm(-)* strain of E. coli, plasmid DNA isolated, and the 60 bp PstI-StuI fragment encoding the modified IgG1 hinge region was isolated and used to replace the corresponding fragment in pdHL7- KS-γ4.

25   **[0194]**   For comparison, the IgG4 form with a mutation in the hinge region (Angal et al., ibid.) was constructed as follows. An oligonucleotide duplex encoding the γ4 hinge with the serine to proline substitution, and a 5' *PstI* sticky end and a 3' *StuI* blunt end, was designed as follows:

PstI   E   S   K   Y   G   P   P   C   P   <u>P</u>   C   P (SEQ ID NO: 35)

30   GAG TCC AAA TAT GGT CCC CCA TGC CCA <u>CCT</u> TGC CCA GGTAAG

    ACGT CTC AGG TTT ATA CCA GGGGGT ACG GGT GGA ACG GGT CCATTC

StuI

CCAACCC*AGG* (complement of SEQ ID NO: 36)

GGTTGGG*TCC* (SEQ ID NO: 36)

5

[0195]   This oligonucleotide duplex was used to replace the corresponding DNA fragment in pdHL7-KS-γ4 to give pdHL7-KS- γ4(S to P).

[0196]   The pdHL7- KS-γ4, pdHL7- KS-γ4h, and pdHL7- KS-γ4(S to P) plasmids were transfected into mammalian cells according to standard procedures, for example,

10   as described in Lo et al., (1998; Protein Engineering 11:495-500). From the supernatants of transfected cells, the antibody proteins encoded by pdHL7- KS-γ4, pdHL7- KS-γ4h, and pdHL7- KS-γ4(S to P) were purified and characterized by SDS gel electrophoresis in which reduced and non-reduced samples were compared.

[0197]   By examining non-reduced molecules, it was found that the KS-γ4

15   antibody population existed as about 50% HL "half-molecules" and 50% H_2L_2 molecules. In contrast, the KS-γ4h antibody population and the KS-γ4 (S to P) antibody population existed almost entirely as H_2L_2 molecules. The proportion of HL half-molecules was about the same in the KS-γ4h antibody population and the KS-γ4 (S to P) antibody population. When reduced molecules were examined, the pattern of

20   heavy and light chains seen with KS-γ4, KS-γ4h, and KS-γ4(S to P) were indistinguishable.

Example 16: Expression of hybrid isotype antibody fusion proteins using components of IgG1 and IgG4.

[0198]   The plasmid pdHL7- KS-γ4-IL2 was described in Gillies et al. (Cancer

25   Research [1999] 59:2159). This plasmid encodes an antibody fusion protein with V regions that recognize the EpCAM antigen and contain the heavy chain of IgG4 with interleukin-2 fused at its C-terminus.

[0199]   By recombinant DNA procedures analogous to those used in Example 15, the plasmids pdHL7- KS-γ4h-IL2 and pdHL7- KS-γ4 (S to P)-IL2 were constructed.

30   The plasmids pdHL7- KS-γ4-IL2, pdHL7- KS-γ4h-IL2 and pdHL7- KS-γ4 (S to P)-IL2 transfected into mammalian cells, and the corresponding proteins were expressed and purified according to standard procedures, for example, as described in Lo et al.

(ref). From the supernatants of transfected cells, the fusion proteins encoded by

pdHL7- KS-γ4-IL-2, pdHL7- KS-γ4h-IL-2, and pdHL7- KS-γ4(S to P)-IL-2 were

purified and characterized by SDS gel electrophoresis in which reduced and non-

reduced samples were compared.

5   [0200]   By examining non-reduced molecules, it was found that the KS-γ4-IL-2

fusion protein population existed as about 50% HL "half-molecules" and 50% H_2L_2

molecules. In contrast, the KS-γ4h-IL-2 fusion protein population and the KS-γ4 (S

to P)-IL-2 fusion protein population existed almost entirely as H_2L_2 molecules. The

proportion of HL half-molecules was about the same in the KS-γ4h-IL-2 fusion

10   protein population and the KS-γ4(S to P)-IL-2 fusion protein population. When

reduced molecules were examined, the pattern of heavy and light chains seen with

KS-γ4-IL-2, KS-γ4h-IL-2, and KS-γ4(S to P)-IL-2 were indistinguishable.

Example 17: Expression of hybrid isotype Fc fusion proteins using components of
IgG1 and IgG4.

15   [0201]   To create an set of plasmids for expression of fusion proteins containing a

hinge region, a CH2 and CH3 domain, and a non-Ig moiety, in which the Ig moieties

were derived from IgG4 and IgG1, the following steps were undertaken.

[0202]   First, using procedures analogous to those described in Example 1, an

expression vector encoding the Fc region from IgG4 was created by replacing the

20   IgG1-derived DNA sequences of pdCs-huFcγ1 (Lo et al., [1998] Protein Engineering

11:495-500) with sequences encoding the corresponding part of IgG4. Specifically,

the following oligonucleotide

                E   S   K   Y   G   P   P   C   P   S   C (SEQ ID NO:

25   37)

C TTA AGC GAG TCC AAA TAT GGT CCC CCA TGC CCA TCA TGC (SEQ ID NO:

38)

              which encodes an AflII site at its 5' end, was used as a 5' primer to amplify a

30   DNA segment encoding the IgG4 hinge, CH2, and CH3 regions. The 3' primer

contained a XhoI site at its 5' end, analogously to the primer used in Example 1 to

amplify the IgG2 Fc region. The resulting AflII-XhoI fragment was inserted into XhoI+AflII-cut pdCs-huFcγ1 to create pdCs-huFcγ4.

[0203]   To facilitate the insertion of nucleic acids encoding non-IgG moieties at the C-terminus of Fcγ4, a SmaI site was created by introducing the following Leu to

5   Pro change near the C-terminus of the Fcγ4 coding region in pdCs-huFcγ4, as follows:

S   L   G   K   STOP   S   P   G   K   STOP
   (SEQ ID NO: 39)   (SEQ ID NO: 40)
TCT CTG GGT AAA TGA   was changed to   TCC CCG GGT AAA TGA.
10   (SEQ ID NO: 41)   (SEQ ID NO: 42)

[0204]   Standard site-directed mutagenesis techniques were used to introduce the SmaI site into pdCs-huFcγ4.

[0205]   To create a plasmid, termed pdCs-huFcγ4h, encoding the modified IgG1

15   hinge followed by the IgG4 CH2 and CH3 domains, the StuI-XhoI fragment of pdCs-huFcγ2h (Example 1), which encodes the IgG2 CH2 and CH3 domains, was replaced with the corresponding fragment from pdCs-huFcγ4. In this construction, each parental plasmid was derived from a *dcm(-)* strain of E. coli. The pdCs-huFcγ4 plasmid was completely digested with XhoI and partially digested with StuI, since

20   there is an additional StuI site in the γ4-encoding DNA, to yield fragments of about 300, 500 and 800 base pairs. The approximately 800 base pair fragment was used to replace the corresponding fragment in pdCs-huFcγ2h.

[0206]   An IFNβ cDNA was cloned by PCR using sense primer CCCGGGT ATG AGC TAC AAC TTG CTT GGA TTC (SEQ ID NO: 43), where ATG is the N-

25   terminal residue of the mature protein and CCCGGG is an introduced SmaI restriction site, and reverse primer CTCGAG TCA GTT TCG GAG GTA ACC TGT AAG (SEQ ID NO: 44), where TCA is the anticodon of the translation stop codon and CTCGAG is an introduced XhoI restriction site. The template DNA was pLG117R (Taniguchi et al., [1980] Proc. Nat. Acad. Sci. USA 77:5230-⁵233) and was

30   purchased from the American Type Culture Collection (ATCC number 31903). After sequence verification, the cloned SmaI-XhoI fragment was ligated to the SmaI and XhoI sites of the pdCs-huFcγ4 expression vector to give pdCs- huFcγ4-IFNβ. An

analogous pdCs- huFcγ4h-IFNβ expression plasmid was also constructed by similar methods.

[0207]   To construct the pdCs- huFcγ4(S to P)-IFNβ expression plasmid, an oligonucleotide duplex encoding the γ4 hinge with the serine to proline substitution, and a 5' AflIII sticky end and a 3' StuI blunt end was synthesized as follows:

AflII   E   S   K   Y   G   P   P   C   P   P   C   P (SEQ ID NO: 45)

    TTA AGC GAG TCC AAA TAT GGT CCC CCA TGC CCA CCT TGC CCA GGT
        G CTC AGG TTT ATA CCA GGG GGT ACG GGT GGA ACG GGT CCA

              StuI
AAGCCAACCCAGG (SEQ ID NO: 46)
TTC GGTTGGGTCC (complement of SEQ ID NO: 46)

[0208]   This DNA was used to replace the corresponding DNA fragment in pdCs-Fc-g4-IFNβ to give pdCs-huFcγ4(S to P)-IFNβ.

[0209]   The plasmids pdCs-huFcγ4-IFNβ, pdCs-huFcγ4h-IFNβ, and pdCs-huFcγ4(S to P)-IFNβ were each transfected into mammalian cells. The expressed Fc-containing proteins were purified and examined by reducing and non-reducing SDS gel electrophoresis. It was found that a significant proportion of the huFcγ4-IFNβ protein expressed from mammalian cells was monomeric half-molecules rather than dimeric, normal antibodies. However, the expressed huFcγ4h-IFNβ, and huFcγ4(S to P)-IFNβ fusion proteins were almost entirely correctly assembled dimers. For both the huFcγ4h-IFNβ, and huFcγ4(S to P)-IFNβ fusion proteins, the proportion of monomer was about the same.

[0210]   Taken together, the results of Examples 15, 16, and 17 indicate that hybrid isotype antibodies and Ig fusion proteins consisting primarily of IgG4 but having the modified IgG1 hinge have superior assembly properties as compared to corresponding proteins derived entirely from IgG4. In addition, the results of Examples 15-17, in combination with other Examples, illustrate that the improved assembly of hybrid isotype proteins can be manifested in several different ways. For example, in some

cases a hybrid isotype antibody or fusion protein shows reduced aggregation, as compared to a corresponding single-isotype antibody or Ig fusion protein; and in other cases the hybrid isotype antibody or fusion protein shows enhanced correct oligomerization, as compared to a corresponding single-isotype antibody or Ig fusion

5   protein.

Example 18: Expression of hybrid isotype Fc fusion proteins using components of IgG1 and IgG4.

[0211]   To generate an Fc-erythropoietin fusion protein that is minimally aggregated when expressed from mammalian cells, the following expression plasmid

10   was constructed using standard molecular biology techniques. An XmaI-XhoI DNA fragment containing a form of the human erythropoietin coding sequence with mutations resulting in the amino acid substitutions His32Gly, Cys33Pro, Trp88Cys, and Pro90Ala, as disclosed in WO01/36489, was used. The corresponding protein sequence is shown in SEQ ID NO: 47:

15   ```
APPRLICDSRVLERYLLEAKEAENITTGCAEGPSLNENITVPDTKVNFYAWKRMEVGQQAVEVWQGLAL
LSEAVLRGQALLVNSSQPCEGLQLHVDKAVSGLRSLTTLLRALGAQKEAISPPDAASAAPLRTITADTF
RKLFRVYSNFLRGKLKLYTGEACRTGDR
```

[0212]     This XmaI-XhoI DNA fragment was inserted into a plasmid vector that

20     encodes a hinge region from IgG1 and a CH2 and CH3 region from IgG2 that was essentially identical to the vector constructed in Example 1, except that there were two sets of mutations that resulted in amino acid substitutions in the region of the CH3 C-terminus, such that the sequence at the junction of the CH3 C-terminus and the Epo N-terminus is as follows:

25                         .... TQKSATATPGA-APPRLI ....(SEQ ID NO: 48)

[0213]     The first set of mutations, which change the sequence KSLSLSPG (SEQ ID NO: 49) of the IgG2 CH3 region to KSATATPG (SEQ ID NO: 45), is disclosed in U.S. Patent Application Serial No. 60/280,625.  The effect of the substitution of Leu-Ser-Leu-Ser (position 3 to position 6 of SEQ ID NO: 49) with Ala-Thr-Ala-Thr

30     (position 3 to position 6 of SEQ ID NO: 50) is to remove potential human non-self T-cell epitopes that may arise because the junction between human Fc and human erythropoietin contains non-self peptide sequences.  The second set consisting of the single amino acid substitution K to A at the C-terminal amino acid of the CH3 region, is disclosed in U.S. Patent Application Serial No. 09/780,668.

[0214]   The resulting plasmid was transfected into NS/0 cells and the Fc-Epo fusion protein was expressed and purified according to the procedures of Examples 1 and 2. After purification based on binding to protein A, the huFcγ2h-huEpo protein containing the IgG2 CH3 and erythropoietin substitutions described above was

5   characterized by size exclusion chromatography and found to consist of 97% monomer and 90% monomer in two independent preparations. The huFcγ2h-huEpo protein containing the IgG2 CH3 and erythropoietin substitutions described above was found to be about as active, on a molar basis, as human erythropoietin in a cell-based assay that measured the ability of an erythropoietin protein to stimulate TF-1

10   cell division. The assay was performed as described in WO01/36489.

[0215]   In addition, fusions of non-mutant human erythropoietin to the C-terminus of an Fc region consisting of either IgG1(hinge-CH2-CH3), IgG2(hinge-CH2-CH3), or IgG1(hinge)-IgG2(CH2-CH3) were characterized. Expression plasmids comprising non-mutant human Fc sequences and non-mutant erythropoietin

15   sequences were constructed analogously to the plasmid described above and in Example 1. NS/0 cells were transfected with the Fcγ1-Epo, Fcγ2-Epo, and Fcγ2h-Epo expression plasmids, and stable clones were isolated after screening an approximately equal number of clones for each plasmid. The best-producing clones yielded 50 μg/ml for Fcγ1-Epo, 20 μg/ml for Fcγ2-Epo, and 120 μg/ml for Fcγ2h-Epo.

20                                         **Equivalents**

[0216]   The invention may be embodied in other specific forms without departing from the spirit or essential characteristics thereof. The foregoing embodiments are therefore to be considered in all respects illustrative rather than limiting on the invention described herein. Scope of the invention is thus indicated by the appended

25   claims rather than by the foregoing description, and all changes which come within the meaning and range of equivalency of the claims are intended to be embraced therein.


                                **Incorporation by Reference**

30   [0217]   All patents, patent applications, and scientific publications mentioned herein above are incorporated by reference into this application in their entirety.

What is claimed is:

1       1.  A fusion protein comprising an immunoglobulin moiety fused to a non-
2    immunoglobulin moiety, wherein said immunoglobulin moiety comprises a first
3    domain from a first antibody isotype and a second domain from a second antibody
4    isotype.

1       2.  A fusion protein of Claim 1, wherein said immunoglobulin region comprises a
2    hinge region from a first antibody isotype and a constant region from a second
3    antibody isotype.

1       3.  The fusion protein of Claim 2, wherein said constant region is a CH2 domain.

1       4.  The fusion protein of Claim 3, wherein said CH2 domain is from a human
2    IgG2 heavy chain, and said hinge region contains three or fewer cysteine residues.

1       5.  The fusion protein of Claim 3, wherein said CH2 domain is from a human
2    IgG4 heavy chain.

1       6.  The fusion protein of Claim 2, wherein the hinge region is a non-IgG2 hinge
2    region.

1       7.  The fusion protein of Claim 2, wherein the hinge region is derived from
2    human IgG1.

1       8.  The fusion protein of Claim 3-6, wherein the hinge region has two or fewer
2    cysteines.

1       9.  The fusion protein of Claim 1, wherein said immunoglobulin domain lacks an
2    antigen-binding site.

1       10. The fusion protein of Claim 1, wherein said immunoglobulin domain
2    comprises an antigen-binding site.

1       11. The fusion protein of Claim 1, wherein the non-Ig moiety is fused by genetic
2    engineering to the C-terminus of a heavy chain of the Ig domain.

1       12. The fusion protein of Claim 1, wherein the non-Ig moiety is fused by genetic
2    engineering to the N-terminus of a heavy chain of the Ig domain.

1      13. The fusion protein of Claim 1, wherein the non-Ig moiety is fused to a light

2      chain polypeptide.

1      14. The fusion protein of Claim 2, wherein the hinge region is from a human IgA.

1      15. The fusion protein of Claim 1, wherein said first immunoglobulin domain is a

2      CH2 domain and said second immunoglobulin domain is a CH3 domain.

1      16. The fusion protein of Claim 15, wherein the first antibody isotype is an IgG

2      and the second antibody isotype is an IgM or an IgA.

1      17. An antibody or Ig fusion protein comprising an IgG2 antibody moiety in

2      which the IgG2 hinge has been mutated two contain two cysteines.

1      18. An immunoglobulin moiety comprising a V domain directed against a tumor-

2      associated antigen, said immunoglobulin moiety comprising a first domain from a

3      first antibody isotype and a second domain from a second antibody isotype.

1      19. The protein of claim 18, comprising an inactive Fc receptor I binding site and

2      a hinge region with three or fewer cysteines.

1      20. A nucleic acid encoding a fusion protein of Claim 1, 17, or18.

1      21. A stably transfected cell expressing a protein of Claim 1, 17, or18.

1      22. A method for improving the assembly of an antibody or Ig fusion protein, the

2      method comprising the steps of:

1      a.          replacing the hinge region of said protein with a different hinge region;

2      and,

3      b.          testing the assembly of the altered protein

4      23. The method of Claim 22, wherein said protein and said altered protein are

5      produced by genetic engineering techniques.

1      24. The fusion protein of claim 1, wherein the immunoglobulin moeity comprises

2      an Fc heavy chain region and the non-immunoglobulin moeity comprises an

3      erythropoietin molecule.

ι      ̲ ̲ ̲. ̲ ̲ nucleic acid encoding the fusion protein of claim 24.

1      26. The fusion protein of claim 1, wherein the non-immunoglobulin moeity

2      comprises an erythropoietin molecule.

1      27. A method for improving the production of an antibody or Ig fusion protein

2      from a cell, the method comprising the steps of:

3              a.  replacing the hinge region of said protein with a different hinge region;

4      and

5              b.  testing the production of the altered protein. ·

1      28. The method of Claim 27, wherein said protein and said altered protein are

2      produced by genetic engineering techniques.

Figure 1.

A.



C.



B.



D.

Figure 2.

A.



B.



C.

Figure 3.

A.

C.

B.

D.

E.

Figure 4.

## SEQUENCE LISTING

<110> Lexigen Pharmaceuticals Corp.
     Gillies, Stephen
     Way, Jeffrey

<120> Expression Technology for Proteins Containing a Hybrid Isotype
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<151> 2001-03-07

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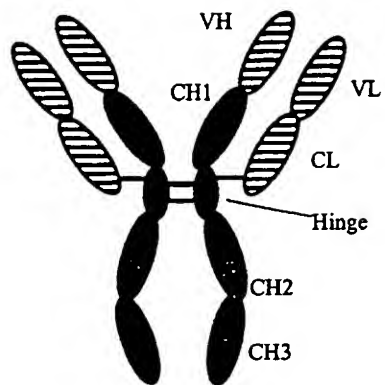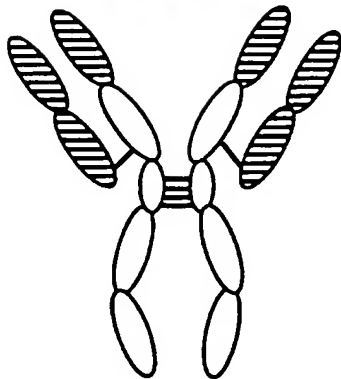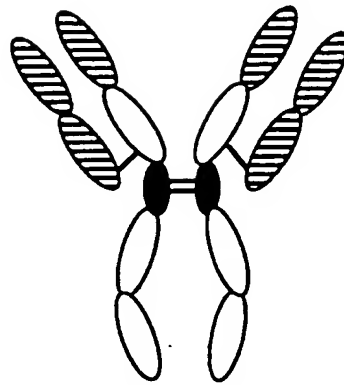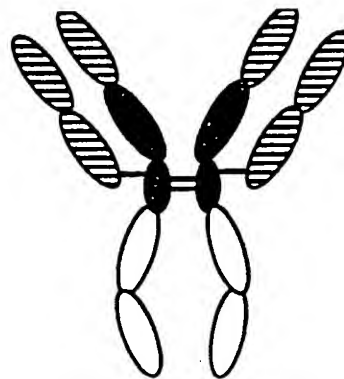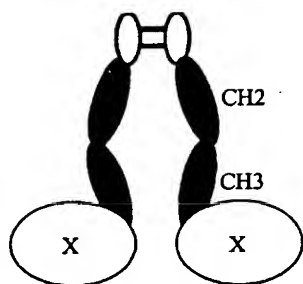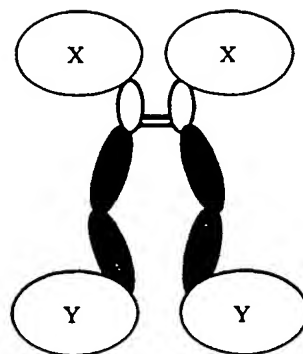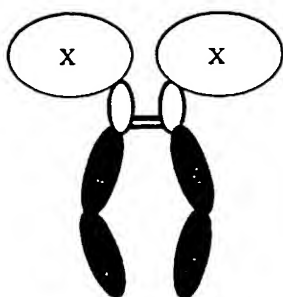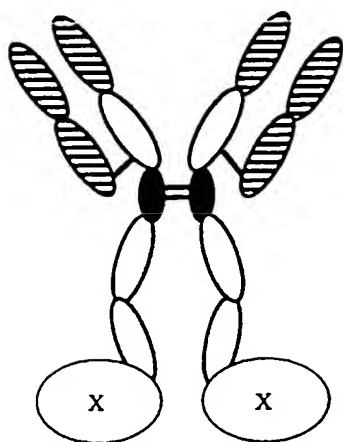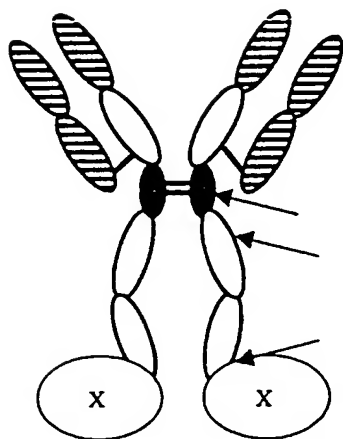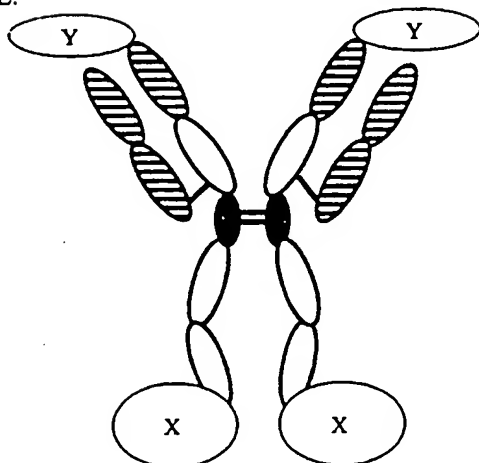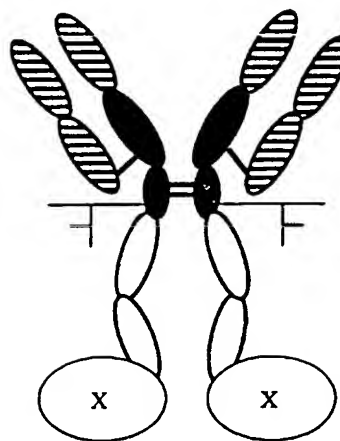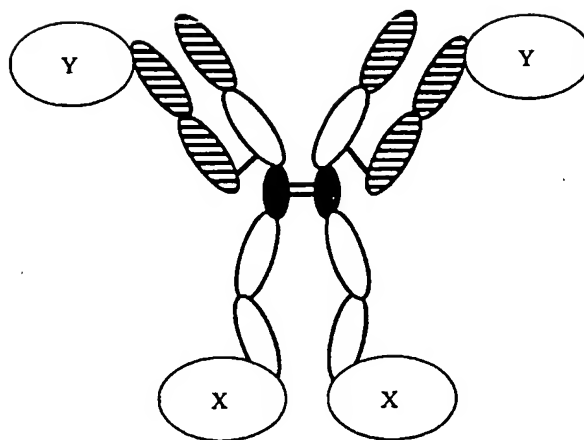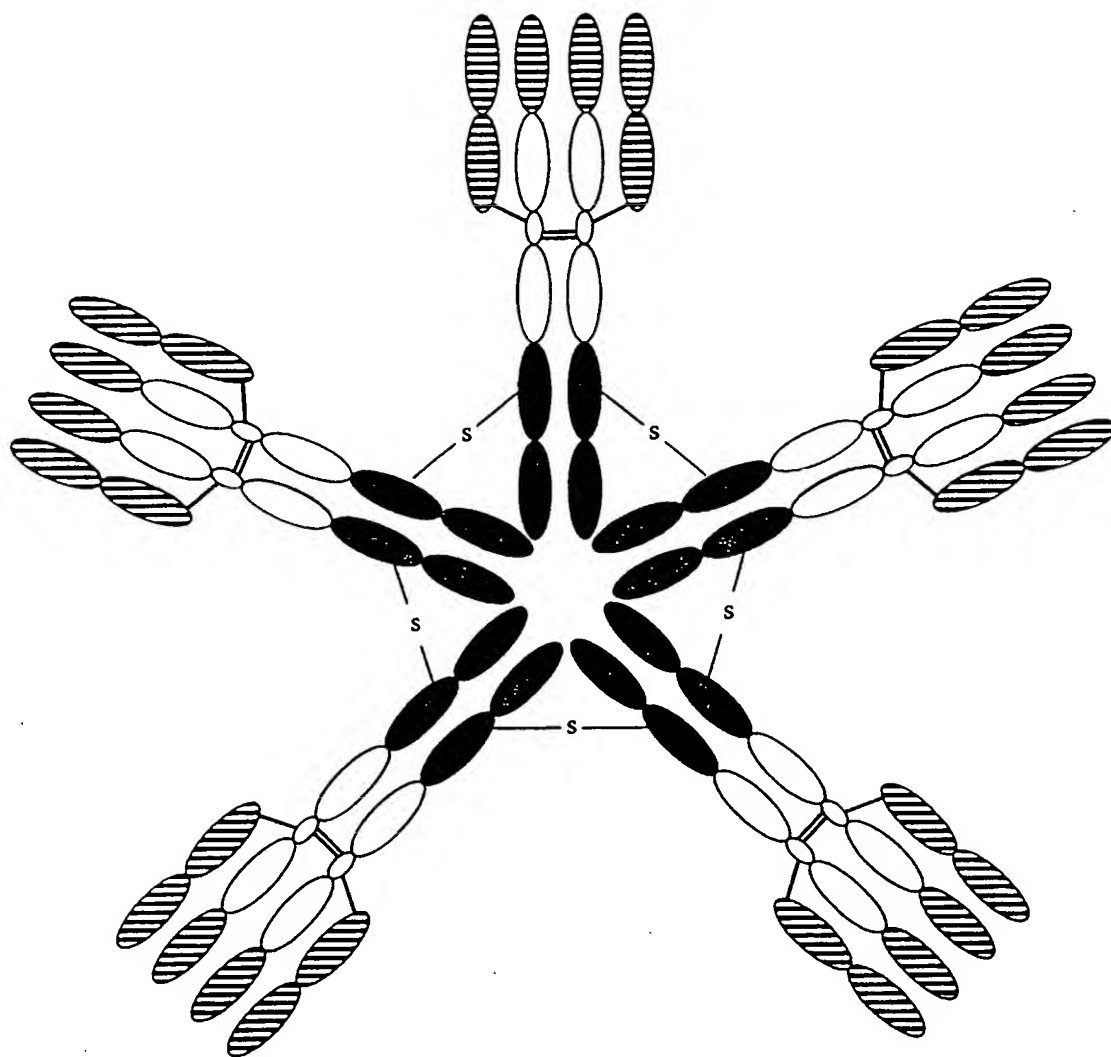
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ct                                                                     62


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<400>   16

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1               5                   10                  15

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1   5   10   15

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            20   25   30

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<223> reverse primer for gamma 1 hinge region

<400> 23
cagctggggc ctgtccctg   19

<210> 24
<211> 10
<212> DNA
<213> artificial sequence

<220>
<223> sequence in pDHL2-huKS antibody

<400> 24
gggtaaatga   10

<210> 25
<211> 89
<212> DNA
<213> artificial sequence

<220>
<223> IgA1 hinge exon

<400> 25
cttaagtccc tcaactccac ctaccccatc tccctcaact ccacctaccc catctccctc   60

atgctgccac ggtaagccag cccaggcct   89

<210> 26
<211> 21
<212> PRT
<213> artificial sequence

<220>
<223> IgA1 hinge region

<400> 26

Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser
1   5   10   15

Pro Ser Cys Cys His
            20

<210> 27
<211> 85
<212> DNA
<213> artificial sequence

<220>
<223> top replacement strand

<400> 27

ttaagtcccc caactccacc taccccatct ccctcaactc cacctacccc atctccctca   60

tgctgccacg gtaagccagc ccagg   85

<210> 28
<211> 81
<212> DNA
<213> artificial sequence

<220>
<223> bottom replacement strand

<400> 28
cctgggctgg cttaccgtgg cagcatgagg gagatggggt aggtggagtt gagggagatg   60

gggtaggtgg agttgaggga c   81

<210> 29
<211> 33
<212> DNA
<213> artificial sequence

<220>
<223> primer for IgM CH3 and CH4

<400> 29
gcagccggcc ctgagccttg gcttcccaga gcg   33

<210> 30
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> primer for IgM CH3 and CH4

<400> 30
gctcccgggt cagtagcagg tgccagctgt gtcg   34

<210> 31
<211> 33
<212> DNA
<213> artificial sequence

<220>
<223> primer for IgM for mutating the C-terminal most Cys to Ser

<400> 31
gcagccggcc ctgagccttg gcttcccaga gcg   33

<210> 32
<211> 34
<212> DNA
<213> artificial sequence

<220>

... primer for IgM for mutating the C-terminus Cys to a Ser

<400> 32
gctcccgggt cagtagctgg tgccagctgt gtcg   34

<210> 33
<211> 460
<212> PRT
<213> artificial sequence

<220>
<223> constant region for IgG1-IgM hybrid

<400> 33

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1   5   10   15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20   25   30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35   40   45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50   55   60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65   70   75   80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85   90   95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100   105   110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115   120   125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130   135   140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145   150   155   160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165   170   175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180   185   190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195   200   205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Asp
    210   215   220

Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro Ser Phe Ala Ser
225   230   235   240

```
. . ... ...  Thr Lys Ser Thr Lys Leu Thr Cys Leu Val Thr Asp Leu
                245             250             255

Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg Gln Asn Gly Glu
            260             265             270

Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His Pro Asn Ala Thr
            275             280             285

Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp Asp Trp Asn Ser
    290             295             300

Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp Leu Pro Ser Pro
305             310             315             320

Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala Leu His Arg Pro
                325             330             335

Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu
            340             345             350

Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser Pro Ala Asp Val
            355             360             365

Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr
    370             375             380

Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe
385             390             395             400

Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp Asn Thr Gly Glu
            405             410             415

Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro Asn Arg Val Thr
            420             425             430

Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr Leu Tyr Asn Val
        435             440             445

Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
    450             455             460

<210>  34
<211>  7
<212>  PRT
<213>  artificial sequence

<220>
<223>  peptide sequence in the IgG1-IgM hybrid

<400>  34

Ala Ser Ile Cys Glu Asp Asp
1               5

<210>  35
<211>  12
<212>  PRT
<213>  artificial sequence

<220>
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...... IgG4 hinge region with a Ser to Pro mutation

<400> 35

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1   5   10

<210> 36
<211> 56
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide duplex

<400> 36
acgtctcagg tttataccag ggggtacggg tggaacgggt ccattcggtt gggtcc   56

<210> 37
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> IgG4 hinge

<400> 37

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys
1   5   10

<210> 38
<211> 40
<212> DNA
<213> artificial sequence

<220>
<223> primer for IgG4 hinge, CH2 and CH3 regions

<400> 38
cttaagcgag tccaaatatg gtcccccatg cccatcatgc   40

<210> 39
<211> 4
<212> PRT
<213> artificial sequence

<220>
<223> peptide sequence near the C-terminus of the Fc gamma 4 coding
      region

<400> 39

Ser Leu Gly Lys
1

<210> 40
<211> 4
<212> PRT

<213> artificial sequence

<220>
<223> peptide sequence near the C-terminus of the Fc gamma 4 coding reg
      ion with a Leu to Pro mutation

<400> 40

Ser Pro Gly Lys
1

<210> 41
<211> 15
<212> DNA
<213> artificial sequence

<220>
<223> sequence near the C-terminus of the Fc gamma 4 coding region

<400> 41
tctctgggta aatga   15

<210> 42
<211> 15
<212> DNA
<213> artificial sequence

<220>
<223> sequence near the C-terminus of the Fc gamma 4 coding region with
       a Leu to Pro mutation

<400> 42
tccccgggta aatga   15

<210> 43
<211> 31
<212> DNA
<213> artificial sequence

<220>
<223> IFN beta sense primer

<400> 43
cccgggtatg agctacaact tgcttggatt c   31

<210> 44
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> IFN beta reverse primer

<400> 44
ctcgagtcag tttcggaggt aacctgtaag   30

<210> 45

<212> PRT
<213> artificial sequence

<220>
<223> Fc gamma 4 hinge region with a Ser to Pro mutation

<400> 45

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1   5   10

<210> 46
<211> 58
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide duplex encoding the Fc gamma 4 containing the Ser
      to Pro mutation

<400> 46
ttaagcgagt ccaaatatgg tcccccatgc ccaccttgcc caggtaagcc aacccagg   58

<210> 47
<211> 166
<212> PRT
<213> artificial sequence

<220>
<223> protein sequence for a mutated form of erythropoietin protein

<400> 47

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
1   5   10   15

Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu Gly
            20   25   30

Pro Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
            35   40   45

Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
    50   55   60

Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65   70   75   80

Leu Val Asn Ser Ser Gln Pro Cys Glu Gly Leu Gln Leu His Val Asp
            85   90   95

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
            100   105   110

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
            115   120   125

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
            130   135   140

Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
145   150   155   160

Cys Arg Thr Gly Asp Arg
                165

<210> 48
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> sequence at the junction of CH3-Epo

<400> 48

Thr Gln Lys Ser Ala Thr Ala Thr Pro Gly Ala Ala Pro Pro Arg Leu
1   5   10   15

Ile

<210> 49
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> IgG2 CH3 sequence

<400> 49

Lys Ser Leu Ser Leu Ser Pro Gly
1   5

<210> 50
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> IgG2 CH3 region

<400> 50

Lys Ser Ala Thr Ala Thr Pro Gly
1   5